

PCTWORLD INTELLECTUAL PROPERTY ORGANIZATION
International Bureau

INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(51) International Patent Classification ⁷ : C12Q 1/68	A2	(11) International Publication Number: WO 00/52204 (43) International Publication Date: 8 September 2000 (08.09.00)
(21) International Application Number: PCT/IB00/00367 (22) International Filing Date: 22 February 2000 (22.02.00) (30) Priority Data: 60/121,124 22 February 1999 (22.02.99) US (63) Related by Continuation (CON) or Continuation-in-Part (CIP) to Earlier Application US 60/121,124 (CON) Filed on 22 February 1999 (22.02.99) (71)(72) Applicant and Inventor: ORNTOFT, Torben, F. [DK/DK]; Dept. Clin. Biochem, Skejby Sygehus, DK-8200 Aarhus N (DK). (74) Agent: JANSSEN, Bernd; Uexküll & Stolberg, Beselerstrasse 4, D-22607 Hamburg (DE).		(81) Designated States: AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU, CZ, DE, DK, DM, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, ARIPO patent (GH, GM, KE, LS, MW, SD, SL, SZ, TZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG). Published <i>Without international search report and to be republished upon receipt of that report.</i>
(54) Title: GENE EXPRESSION IN BLADDER TUMORS (57) Abstract Methods for analyzing tumor cells, particularly bladder tumor cells employ gene expression analysis of samples. Gene expression patterns are formed and compared to reference patterns. Alternatively gene expression patterns are manipulated to exclude genes which are expressed in contaminating cell populations. Another alternative employs subtraction of the expression of genes which are expressed in contaminating cell types. These methods provide improved accuracy as well as alternative basis for analysis from diagnostic an prognostic tools currently available.		

FOR THE PURPOSES OF INFORMATION ONLY

Codes used to identify States party to the PCT on the front pages of pamphlets publishing international applications under the PCT.

AL	Albania	ES	Spain	LS	Lesotho	SI	Slovenia
AM	Armenia	FI	Finland	LT	Lithuania	SK	Slovakia
AT	Austria	FR	France	LU	Luxembourg	SN	Senegal
AU	Australia	GA	Gabon	LV	Latvia	SZ	Swaziland
AZ	Azerbaijan	GB	United Kingdom	MC	Monaco	TD	Chad
BA	Bosnia and Herzegovina	GE	Georgia	MD	Republic of Moldova	TG	Togo
BB	Barbados	GH	Ghana	MG	Madagascar	TJ	Tajikistan
BE	Belgium	GN	Guinea	MK	The former Yugoslav Republic of Macedonia	TM	Turkmenistan
BF	Burkina Faso	GR	Greece	ML	Mali	TR	Turkey
BG	Bulgaria	HU	Hungary	MN	Mongolia	TT	Trinidad and Tobago
BJ	Benin	IE	Ireland	MR	Mauritania	UA	Ukraine
BR	Brazil	IL	Israel	MW	Malawi	UG	Uganda
BY	Belarus	IS	Iceland	MX	Mexico	US	United States of America
CA	Canada	IT	Italy	NE	Niger	UZ	Uzbekistan
CF	Central African Republic	JP	Japan	NL	Netherlands	VN	Viet Nam
CG	Congo	KE	Kenya	NO	Norway	YU	Yugoslavia
CH	Switzerland	KG	Kyrgyzstan	NZ	New Zealand	ZW	Zimbabwe
CI	Côte d'Ivoire	KP	Democratic People's Republic of Korea	PL	Poland		
CM	Cameroon	KR	Republic of Korea	PT	Portugal		
CN	China	KZ	Kazakhstan	RO	Romania		
CU	Cuba	LC	Saint Lucia	RU	Russian Federation		
CZ	Czech Republic	LI	Liechtenstein	SD	Sudan		
DE	Germany	LK	Sri Lanka	SE	Sweden		
DK	Denmark	LR	Liberia	SG	Singapore		
EE	Estonia						

GENE EXPRESSION IN BLADDER TUMORS

This application claims the benefit of U.S. Provisional Application No. 60/121,124, filed February 22, 1999, which is hereby incorporated by reference in its entirety.

5 TECHNICAL FIELD OF THE INVENTION

This invention is related to the field of cancer diagnosis and treatment. In particular it is related to the use of gene expression to categorize and detect tumors.

BACKGROUND OF THE INVENTION

10 The building of large databases containing human genome sequences is the basis for studies of gene expressions in various tissues during normal physiological and pathologic conditions. Constantly (constitutively) expressed sequences as well as sequences whose expression is altered during disease processes are important for our understanding of cellular properties, and for
15 the identification of candidate genes for future therapeutic intervention. As the number of known genes and ESTs build up in the databases, array-based simultaneous screening of thousands of genes is necessary to obtain a profile of transcriptional behaviour, and to identify key genes that, either alone or in combination with other genes, control various aspects of cellular life. One

MISSING AT THE TIME OF PUBLICATION

Still another object of the invention is to provide a method of identifying a tissue sample as urothelial.

Yet another object of the invention provides a method of determining an expression pattern of a bladder tissue sample independent of the proportion of submucosal, muscle, and connective tissue cells present.

These and other objects of the invention are achieved by providing one or more of the embodiments described below. In one embodiment a method is provided of determining an expression pattern of a cell sample independent of the proportion of submucosal, smooth muscle, or connective tissue cells present. Expression is determined of one or more genes in a sample comprising cells. The one or more genes exclude genes which are expressed in the submucosal, muscle, and connective tissue. A pattern of expression is formed for the sample which is independent of the proportion of submucosal, muscle, and connective tissue cells in the sample.

In another aspect of the invention a method of determining an expression pattern of a cell sample is provided. Expression is determined of one or more genes in a sample comprising cells. A first pattern of expression is thereby formed for the sample. Genes which are expressed in submucosal, smooth muscle, or connective tissue cells are removed from the first pattern of expression, forming a second pattern of expression which is independent of the proportion of submucosal, smooth muscle, or connective tissue cells in the sample.

Another embodiment of the invention provides a method for determining an expression pattern of a urothelium or bladder cancer cell. Expression is determined of one or more genes in a sample comprising urothelium or bladder cancer cells; the expression determined forms a first pattern of expression. A second pattern of expression which was formed using the one or more genes and a sample comprising predominantly submucosal, smooth muscle, or connective tissue cells, is subtracted from the first pattern of expression, forming a third pattern of expression. The third pattern of expression reflects expression of the urothelium or bladder cancer cells

independent of the proportion of submucosal, smooth muscle, or connective tissue cells present in the sample.

5 In another embodiment of the invention a method is provided of detecting an invasive tumor in a patient. A marker is detected in a sample of a body fluid. The body fluid is selected from the group consisting of blood, plasma, serum, urine, ascites fluid, pleural fluid, spinal fluid, sputum, and mucous secretions. The marker is an mRNA or protein expression product of a gene which is more prevalent in submucosal, smooth muscle, or connective tissue than in the body fluid. An increased amount of the marker in the body
10 fluid indicates a tumor which has become invasive in the patient.

In another aspect of the invention a method is provided for diagnosing a bladder cancer. A first pattern of expression is determined of one or more genes in a bladder tissue sample suspected of being neoplastic. The first pattern of expression is compared to a second and third reference pattern of
15 expression. The second pattern is of the one or more genes in normal urothelium and the third pattern is of the one or more genes in bladder cancer. A first pattern of expression which is found to be more similar to the third pattern than the second indicates neoplasia of the bladder tissue sample.

According to yet another aspect of the invention a method is provided
20 for predicting outcome or prescribing treatment of a bladder tumor. A first pattern of expression is determined of one or more genes in a bladder tumor sample. The first pattern is compared to one or more reference patterns of expression determined for bladder tumors at a grade between I and IV. The reference pattern which shares maximum similarity with the first pattern is
25 identified. The outcome or treatment appropriate for the grade of tumor of the reference pattern with the maximum similarity is assigned to the bladder tumor sample.

In another embodiment of the invention a method is provided for determining grade of a bladder tumor. A first pattern of expression is
30 determined of one or more genes in a bladder tumor sample. The first pattern is compared to one or more reference patterns of expression determined for

bladder tumors at a grade between I and IV. The reference pattern which shares maximum similarity with the first pattern is identified. The grade of the reference pattern with the maximum similarity is assigned to the bladder tumor sample.

5 Yet another embodiment of the invention provides a method to determine stage of a bladder tumor. A first pattern of expression is determined of one or more genes in a bladder tumor sample. The first pattern is compared to one or more reference patterns of expression determined for bladder tumors at different stages. The reference pattern which shares
10 maximum similarity with the first pattern is identified. The stage of the reference pattern with the maximum similarity is assigned to the bladder tumor sample.

In still another embodiment of the invention a method is provided for identifying a tissue sample as urothelial. A first pattern of expression is
15 determined of one or more genes in a tissue sample. The first pattern of expression is compared to a second pattern of expression obtained from normal urothelial cells. Similarity between the first and second patterns identifies the tissue sample is urothelial in its origin.

Another aspect of the invention is a method to identify a set of genes
20 useful for diagnosing, predicting outcome, or prescribing treatment of a bladder cancer. A first pattern of expression is determined of one or more genes in a first bladder tissue sample. A second pattern of expression is determined of the one or more genes in a second bladder tissue sample. The first bladder tissue sample is a normal urothelium sample or an earlier stage or lower grade of
25 bladder tumor than the second bladder tissue sample. The first pattern of expression is compared to the second pattern of expression to identify a first set of genes whose expression is increased or decreased in the second bladder tissue sample relative to the first bladder tissue sample. Those genes which are expressed in submucosal, smooth muscle or connective tissue are removed
30 from the first set of genes to produce a second set of genes. Expression of the

second set of genes can be used for diagnosing, predicting outcome, or prescribing treatment of a bladder cancer.

According to yet another aspect of the invention a method is provided for determining an expression pattern of a bladder tissue sample independent of the proportion of submucosal, smooth muscle, or connective tissue cells present. A single-cell suspension of disaggregated bladder tumor cells is isolated from a bladder tissue sample comprising bladder cells, submucosal cells, smooth muscle cells, or connective tissue cells. The expression of one or more genes in the single-cell suspension is determined. A pattern of expression is thus formed for the sample which is independent of the proportion of submucosal, smooth muscle, or connective tissue cells in the bladder tissue sample.

According to still another aspect of the invention a method is provided for screening compounds to identify candidate therapeutic agents for treating bladder cancer. Bladder tumor cells are contacted with a test compound. Gene expression of one or more genes is determined in the bladder tumor cells which have been contacted with the test compound. The one or more genes are ones whose expression changes during the development of a bladder cancer. A test compound is identified as a candidate therapeutic agent if it causes gene expression of at least one of the one or more genes to change to a level which is characteristic of an earlier stage of cancer progression.

The present invention thus provides the art with numerous methods for molecularly assessing bladder cells. The methods aid the art in diagnosing, identifying, classifying, treating, detecting, and treating tumors of the bladder.

BRIEF DESCRIPTION OF THE DRAWINGS AND TABLES

Figure 1 shows a distribution of expression levels in bladder wall tissue expressed in arbitrary units. Only genes scored as present or marginally present are shown.

Figure 2 shows a comparison of intensity differences between a tumor and a pool of tumors of the same stage and grade, and two pools of different

stages and grades. The difference is larger between the pools, demonstrating the validity of using expression patterns to determine stage, grade, prognosis, and treatment regimen.

5 All genes scored as present on two chips (approximately 9000 genes) were compared. Increased genes were compared to increased genes and decreased genes to decreased genes, on two separate chips, followed by plotting of the numerical difference of the medians. A TaGrII tumor compared to the TaGrII pool, and the TaGrII pool to T2GrIV pool (1, 2, 3, 4); T2GrIII to T2GrIII pool, and T2GrIII pool to T2GrIV pool (5, 6, 7, 8); T2GrIV to 10 T2GrIV pool, and T2GrIV pool to TaGrII pool (9, 10, 11, 12). Paired T-test of medians showed a borderline significant difference, with pool vs. pool scoring highest (P-value of 0.07).

Figure 3 shows progression of a bladder cancer from normal urothelium to invasive grade IV tumor. The expression patterns change during the 15 progression, with a great variation in pattern from stage to stage, but also within a stage and even within tumors having the same stage and grade of atypia.

Figure 4 shows the correlation between transcript levels from genes expressed in at least one sample. Fig. 4A demonstrates the repeatability of 20 microarray expression analysis. Duplicate determinations on a normal sample are compared. Fig. 4B is a plot of a pTa tumor vs. the normal pool. Fig. 4C is a plot of an invasive pT2 tumor versus the normal pool. The vast majority of transcripts are present at similar levels in both normal and tumor tissue.

Figure 5 shows dendrograms of tissues based on different clustering 25 methods. Clustering was either based on log-fold change in expression level of genes (Figs. 5A, 5C), or the absolute difference (Figs. 5B, 5D), comparing tumor to a pool of normal samples. Genes used for clustering were either those 10% of the genes that covaried best with progression (A, B), or all 4076 genes that were scored as present in at least one sample (C, D).

30 Figure 6A through 6F show how the pattern of expression changes during progression of bladder cancer based on levels of transcripts in pools of

normal biopsies, superficial pTa tumors grade II, and invasive pT2+grade IV tumors. The curve at the top left portion of each subfigure shows the direction of change in gene expression based on pools of normal urothelium (open circle), superficial pTa tumor (gray circle) and invasive pT2+ tumor (black circle). Fold change in gene expression level was calculated on a probe-to-probe basis using 20 probes per gene and eliminating the highest and lowest outliers (olympic scoring). It is noteworthy that reduced expression is the most common event.

Figure 7 shows a cluster diagram of 9 bladder tumors representing the progression of bladder cancer. Each column represents a tumor preparation, and each row a gene. The diagrams show clustering based on log-fold change from normal urothelium (left diagram) and based on absolute difference from normal urothelium (right diagram). A decreased expression is displayed as shades of cyan, an increased expression as shades of yellow, and no change as black.

The dendrograms at each side show the relation between the different genes. In the middle, distinct functional clusters are identified and members of the clusters are annotated in brief (for full length ID of all genes in the diagram and Genbank numbers see www.mdl.dk/supplementary data). In an effort to identify those genes most indicative of cancer progression a weighting scheme was used to select the 400 genes that covaried best with the different stages of bladder cancer. Gene clustering was based on normalized Euclidean distance (vector angle) calculated between genes or gene cluster centers.

Figure 8 shows the vector angle between pools and individual single cell preparations or biopsies. The numbers refer to patient samples and the stage of each is indicated. Pools are identified as follows: squares, Ta grade I pool; diamonds, Ta grade II pool; circles, T2-4 grade III pool; triangles, T2-4 grade IV pool. The lowest angle for each sample determines the whether the sample is classified as a superficial (Ta or T1) or muscle-invasive tumor (T1-T4).

Figure 9 shows a comparison of Northern blots and oligonucleotide arrays. The samples analyzed were normal pool (Norm), superficial pTaGrI tumor (335), minimally invasive pT1 grade III (901), and invasive pT2 grade III (713). The Northern blots were scanned by densitometry and plotted (solid lines) together with a plot of the level detected on the arrays (dotted lines). The levels of expression ranged from 3-6,000 units (beta -2 microglobulin) to 100-600 units (E-cadherin). The level of transcripts detected was similar with both methods.

Figure 10 shows immunohistochemical staining of the tissue sections used for expression analysis. On each section the protein examined is indicated and the level measured on the oligonucleotide array. Arrows indicate stained urothelial cells in cathepsin E (297 arbitrary units), ApoE (389 units), and CD59 (260 units) stainings, and stained stromal cells or leukocytes in beta2-microglobulin (2481 units) and cystatin C (941 units).

Figure 11 presents a model of gene expression events during the progression of bladder cancer. The top of the figure shows the stages of bladder cancer, and the lower part shows the sequence of transcriptional events. The color cyan identifies reduced expression, yellow increased expression (also indicated by arrows). The figure is based on data from cluster analysis, and combines the different cluster methods.

Table 1 shows genes which were highly expressed in bladder wall. Expression is shown in "connective tissue" which includes muscle and submucosal cells, a TaGr III, a T₂Gr III, and a T₂Gr IV bladder tumor. Genes above the 90th percentile are grouped according to the purported function of the protein.

Table 2A shows high intensity genes in bladder wall compared to single cell solutions and biopsies of tumors.

Table 2B shows expression of genes related to bladder wall.

Table 3 shows the number of genes that are expressed as in the tumor-pool to which the tumor belongs, or altered as in a tumor pool of higher or lower stage or grade.

MISSING AT THE TIME OF PUBLICATION

Several of the tables described above contain lists which include both genes and expressed sequence tags (ESTs). Reference to the "genes" of a table shall be understood to include the gene containing the EST.

DETAILED DESCRIPTION OF THE INVENTION

5 It is a discovery of the present inventor that characteristic patterns of expression of genes can be used to characterize different types of tissue. Thus, for example, gene expression patterns can be used to characterize stages and grades of bladder tumors. Similarly, gene expression patterns can be used to distinguish cells having a bladder origin from other cells. Moreover, gene
10 expression of cells which routinely contaminate bladder tumor biopsies has been identified, and such gene expression can be removed or subtracted from patterns obtained from bladder biopsies. Further, the gene expression patterns of single-cell solutions of bladder tumor cells have been found to be far freer of interfering expression of contaminating muscle, submucosal, and connective
15 tissue cells than biopsy samples.

 Working with human tumor material requires biopsies, and working with RNA requires freshly frozen or immediately processed biopsies. Biopsies inevitably contain many different cell types in addition to cancer cells, such as cells present in blood, connective and muscle tissue, endothelium etc. In the
20 case of DNA studies, microdissection or laser capture are methods of choice, however, the time-dependent degradation of RNA makes it difficult to perform manipulation of the tissue for more than a few minutes. Furthermore, studies of expressed sequences may be difficult on the few cells obtained via microdissection or laser capture, as these may have an expression pattern that
25 deviates from the predominant pattern in a tumor due to intratumoral heterogeneity.

 High-density expression arrays were used to evaluate the impact of bladder wall components in bladder tumor biopsies, and tested preparation of single cell solutions as a means of eliminating the contaminants. The results of
30 these evaluations permitted the design of methods of evaluating bladder

samples without the interfering background noise caused by ubiquitous contaminating submucosal, muscle, and connective tissue cells.

The evaluating assays of the invention may be of any type. While high-density expression arrays can be used, other techniques are also contemplated. These include other techniques for assaying for specific mRNA species, including RT-PCR and Northern Blotting, as well as techniques for assaying for particular protein products, such as ELISA, Western Blotting, and enzyme assays. Gene expression patterns according to the present invention are determined by measuring a gene product of a particular gene, including mRNA and protein. A pattern may be for one or more genes.

Using the results provided in the accompanying figures and tables, a gene is indicated as being expressed if an intensity value of greater than or equal to 21 is shown. Conversely, an intensity value of less than 21 indicates that the gene is not expressed above background levels. Comparison of an expression pattern to another may score a change from expressed to non-expressed, or the reverse. Alternatively, changes in intensity of expression may be scored, either increases or decreases. Any statistically significant change can be used. Typically changes which are greater than 2-fold are suitable. Changes which are greater than 3-fold or 5-fold are highly significant.

A pattern of characteristic expression of just one gene can be useful in characterizing a cell type source or a stage of disease. However, more genes may be usefully analyzed. Useful patterns include expression of at least one, two, three, five, ten, fifteen, twenty, twenty-five, fifty, seventy-five, or one hundred informative genes. As used herein, the phrase "stage-specific reference pattern" refers to a pattern of gene expression characteristic of a given stage of progression in a bladder tumor. A stage-specific reference pattern can include one or more genes listed in Table 4 and/or one or more genes listed in Table 8 and/or one or more genes listed in Table 9 and/or one or more genes listed in Fig. 6.

RNA or protein can be isolated and assayed from a test sample using any techniques known in the art. They can, for example, be isolated from fresh

or frozen biopsy, from formalin-fixed tissue, from body fluids, such as blood, plasma, serum, urine, or sputum.

5 Stage of a bladder tumor indicates how deeply the tumor has penetrated. Superficial tumors are termed Ta, and T₁₋₄ are used to describe increasing degrees of penetration into the muscle. The grade of a bladder tumor is expressed on a scale of I-IV (1-4). The grade reflects the cytological appearance of the cells. Grade I cells are almost normal. Grade II cells are slightly deviant. Grade III cells are clearly abnormal. And Grade IV cells are highly abnormal.

10 As used herein, the reference to genes which are expressed in "submucosal, smooth muscle, or connective tissue" or patterns of expression in "other cell types" can include the expression of one or more of the genes listed in Table 1 and/or one or more of the genes listed in Table 6. The term "connective tissue cell" includes any stromal cell such as fibroblasts,
15 macrophages, mast cells, granulocytes, etc. The data provided herein of expression for submucosal, smooth muscle, and connective tissue can be used in at least three ways to improve the quality of data for a tested sample. The genes identified in the data as expressed can be excluded from the testing altogether or tested but eliminated from the analysis. Alternatively, the
20 intensity of expression of the genes expressed in the submucosal, smooth muscle, and/or connective tissue can be subtracted from the intensity of expression determined for the test tissue.

 Patterns can be compared manually (by a person) or by a computer or other machine. An algorithm can be used to detect similarities and differences.
25 The algorithm may score and compare, for example, the genes which are expressed and the genes which are not expressed. Alternatively, the algorithm may look for changes in intensity of expression of a particular gene and score changes in intensity between two samples. A variety of such algorithms are known in the art. Similarities may be determined on the basis of genes which
30 are expressed in both samples and genes which are not expressed in both samples or on the basis of genes whose intensity of expression are numerically

similar. Differences are considered significant when they are greater than 2-fold, 3-fold or 5-fold from the base value. Alternatively, a mathematical approach can be used to conclude whether differences in the gene expression exhibited by different samples is significant (*see, e.g.*, Golub et al., Science 286, 531 (1999)). One approach to determine whether a sample is more similar to or has maximum similarity with a given condition (*e.g.*, a particular grade or stage of tumor progression) is to compare the Euclidean distances (*see* Golub et al. and Example 6) between the sample and one or more pools representing different conditions for comparison; the pool with the smallest vector angle is then chosen as the most similar to the test sample among the pools compared.

The data collected and disclosed here as "connective tissue" is presumed to contain both smooth muscle and submucosal gene expression as well. Thus it represents the composite expression of those cell types which can typically contaminate a bladder tumor biopsy.

Genes identified as changing in various stages or grades of bladder cancer can be used as markers for drug screening. Thus by treating bladder cancer cells with test compounds or extracts, and monitoring the expression of genes identified as changing in the progression of bladder cancers, one can identify compounds or extracts which change expression of genes to a pattern which is of an earlier stage/grade or even of normal urothelium. As used herein, the reference to expression of genes in "normal urothelium" or "normal urothelial cells" can include one or more genes listed in Table 7.

As demonstrated below, pools of tumors of a similar stage or grade, particularly bladder tumors, can be made and the expression of the pool evaluated. The expression data of the pool can be used to define a stage or grade of tumor. The use of the pool minimizes the variations found from individual tumor to individual tumor of the same grade or stage. The expression data of the pool can then be used as a comparator to which individual tumor samples are compared, in an effort to categorize, prognosticate, and prescribe the tumor samples. The methods described herein for classifying the stage or grade of a tumor can be combined with sequence

analysis of genes whose expression is altered compared to normal tissue in the individual patient. In particular, mutations in key genes such as tumor suppressor genes can help to refine the application of the gene expression results to diagnosis and prognosis.

5 As used herein, the reference to expression of "genes in bladder cancer" or "genes in a bladder tumor" can include one or more genes listed in Table 4 and/or one or more of the genes listed in Table 8 and/or one or more genes listed in Table 9.

10 The above disclosure generally describes the present invention. A more complete understanding can be obtained by reference to the following specific examples which are provided herein for purposes of illustration only, and are not intended to limit the scope of the invention.

EXAMPLE 1

Quantification of gene expression using microarrays

15 Material

Bladder tumor biopsies were sampled from patients after informed consent was obtained, and after removal of the necessary amount of tissue for routine pathological examination. Tumors examined were 335 (stage pTa grade I), 837 (pTa GrII), 901 (pTa GrIII), 320 (pT1 GrIII), 713 (pT2 GrIII).
20 RNA from six different tumors of the same stage and grade was combined to form each pool. Four such pools were prepared (pTa GrI pool, pTa GrII pool, pT2+ GrIII pool, and pT2+ GrIV pool). Normal bladder mucosa biopsies from 36 patients with prostatic hyperplasia or incontinence were pooled (as RNA) to obtain a normal urothelial reference. Single cell solutions were made by
25 disintegrating biopsies on ice with a scalpel and a syringe followed by filtering through a 50 micron filter.

Preparation of mRNA

Total RNA was isolated using the RNeasy B RNA isolation method (WAK-Chemie Medical GMBH). Poly (A)+ RNA was isolated by an oligo-dT
30 selection step (Oligotex mRNA kit from Qiagen).

Preparation of cRNA

One µg mRNA was used as starting material for the cDNA preparation. The first and second strand cDNA synthesis was performed using the SuperScript Choice System (Life Technologies) according to the manufacturer's instructions, except that an oligo-dT primer containing a T7 RNA polymerase promoter site was used. Labeled cRNA was prepared using the MEGAscrip In Vitro Transcription kit (Ambion). Biotin labeled CTP and UTP (Enzo) was used in the reaction together with unlabeled NTP's. Following the IVT reaction, the unincorporated nucleotides were removed using RNeasy columns (Qiagen).

Array hybridization and scanning

Ten µg of cRNA was fragmented at 94°C for 35 min. in a fragmentation buffer containing 40mM Tris-acetate pH 8.1, 100mM KOAc, 30 mM MgOAc. Prior to hybridization, the fragmented cRNA in a 6xSSPE-T hybridization buffer (1M NaCl, 10mM Tris pH 7.6, 0.005% Triton) was heated to 95°C for 5 min and subsequently to 40°C for 5 min before loading onto an Affymetrix probe array cartridge (HuGeneF1 set array, part No. V900160). The probe array was then incubated for 16 h at 40°C at constant rotation (60 rpm). The washing and staining procedure was performed in the Affymetrix Fluidics Station. The probe array was exposed to 10 washes in 6xSSPE-T at 25°C followed by 4 washes in 0.5xSSPE-T at 50°C. The biotinylated cRNA was stained with a streptavidin-phycoerythrin conjugate, 10 µg/ml (Molecular Probes, Eugene, OR) in 6xSSPE-T for 30 min at 25°C followed by 10 washes in 6xSSPE-T at 25°C. The probe arrays were scanned at 560 nm using a confocal laser scanning microscope with an argon ion laser as the excitation source (made for Affymetrix by Molecular Dynamics). The readings from the quantitative scanning were analyzed by the Affymetrix Gene Expression Analysis Software.

Normalization of data

To compare samples, normalization of the data was necessary. For that purpose we compared scaling to total GAPDH intensity (sum of 3', middle,

5'probe sets) of 7000 units with scaling to a total chip intensity (global scaling) of 281850 units (averaging 150 units per probe set). Both gave similar results with scaling factors that differed less than ten percent in a set of experiments. Based on this we chose the global scaling for all experiments. The variation in
5 hybridization intensity following global scaling in biopsies from the bladder wall is shown in Fig.1.

EXAMPLE 2

Interference of bladder wall components on expression profiling of bladder tumor biopsies

10 Biopsies contain epithelial cells that most often are the targets for the studies (e.g., in the identification and characterization of carcinoma cells), and in addition many other cells that contaminate the epithelial cell fraction to a varying extent. The contaminants include histiocytes, endothelial cells, leukocytes, nerve cells, muscle cells etc. Microdissection is the method of
15 choice for DNA examination, but in case of expression studies this procedure is difficult due to RNA degradation during the procedure. Our approach has been to gently remove the epithelium and monitor the expression in the remaining submucosa and underlying connective tissue (the bladder wall). Genes expressed at high or low levels in the bladder wall should be
20 interrogated when performing expression monitoring of the urothelium and urothelial tumors. A similar approach could be used for studies of epithelia in other organs.

We gently scraped off some of the normal urothelium lining the bladder lumen from bladders removed at cystectomy for bladder cancer. Then biopsies
25 were taken from the denuded submucosa and connective tissue, reaching approximately 5 mm into the bladder wall, and immediately disintegrated in guanidinium isothiocyanate. Total RNA was extracted from four different cystectomy specimens, pooled, and poly(A)⁺ mRNA was prepared from the pool followed by conversion to double-stranded cDNA and in vitro
30 transcription into cRNA containing biotin-labeled CTP and UTP.

The labeled sample was hybridized to a set of 4 arrays containing 7074 probe sets for human genes. A total of 1491 of the examined genes (21.1%) were scored as present, and 120 (1.7%) as present but rare. The percentile distribution of the expression intensity was (90%, 1308; 75%, 383; 50%, 163; 25%, 85; 10%, 47). Genes above the 90th percentile (Table 1) were grouped according to the purported function of the protein (Table 1, first column). Many of the highly expressed genes belong to a group of genes that encode proteins involved in transcription and translation, probably reflecting that these genes generally are highly expressed in the various cell types present in the bladder wall, and corresponding to recent data on yeast. Structural proteins such as keratins and proline rich proteins are highly expressed whereas collagen genes are only medium expressed. Extremely high expression is shown by the cystic fibrosis antigen gene, the S100 calcium binding protein, the cystatin B and the cytokeratin 13 genes that are all above 10,000 units.

To evaluate the influence of bladder wall tissue in urothelial tumor biopsies, we monitored the expression level in 3 biopsies from transitional cell carcinomas (one superficially invasive (#733-2) and two muscle invasive (#733-1 and #879-1). The expression intensity in the tumor biopsies of genes that are highly expressed in bladder wall are listed in Table 1. Many genes are expressed to the same magnitude in the tumor biopsies as in bladder wall, 82 genes (5%) were present at a level above 1308 in all samples, and above the 75% percentile of the bladder wall sample intensity (383 units) 210 genes were expressed in all three biopsies as well as in bladder wall. Genes that were not expressed in bladder wall but present in the urothelial biopsies amounted to 196.

Genes that are expressed and genes that are not expressed in bladder wall can both interfere with the interpretation of the expression in a biopsy, and should be interrogated when interpreting expression intensities in urothelial tumor biopsies, as the bladder wall component of a biopsy varies in amount from biopsy to biopsy.

It is remarkable how similarly many genes belonging to the groups encoding metabolically active proteins, transcription and translation related proteins, mitochondrial and nucleoproteins, are expressed in the different samples (Table 1). It seems reasonable to expect that it is incompatible with
5 cellular function to stray from a narrow interval regarding these genes. Although some of the examined cells are malignant of atypia grade IV, which is a severe morphological deviation from normal, the key cellular functions are obviously still under strict control.

Twenty six genes were expressed at an intensity above 1308 in bladder wall and more than five times lower in tumor biopsies. These genes, marked
10 with bold (Table 1), include keratins (7 genes) encoding proteins like keratins type II, 4, and 6. Another prominent group are the genes encoding proline-rich proteins (5 genes). These gene expressions can be used to monitor the amount of bladder wall present in a given biopsy of tumors. The tumor biopsy 879-1
15 obviously has a larger bladder wall component than the other biopsies, as it contains keratin 13 and several other highly expressed bladder wall mRNAs at a low level, but higher than the other specimens (Table 1).

An interesting result was the S100 calcium binding protein A7 gene transcript that was highly expressed in bladder wall and totally absent from the
20 other biopsies (also absent from a number of other examined tumor biopsies from bladder). As all samples were collected with the same procedures, it indicates that this expression is either individual and occurred by chance in the patients from whom we removed the bladder wall biopsies, or, more likely, that the presence of urothelial RNAases degrade this transcript very fast.

25 Bladder tumors have a reduced intercellular cohesion, and easily disintegrate into single cell solutions. To eliminate bladder wall cells from the urothelial tumor cells, five tumors were disintegrated into single cell solutions before extraction of RNA, and compared to three tumors where RNA was extracted from the biopsy directly. We expected that this disintegration
30 procedure might lead to an enrichment of tumor cells and loss of connective tissue cells. Examination of genes highly expressed in bladder wall (Table 2A),

showed a similar expression in single cell solutions of bladder tumor cells compared to biopsies. However, the level was much lower than seen in the bladder wall and raised the question whether the expressed RNAs originate from the bladder wall or from the urothelial cells.

5 To answer this question we examined the expression of genes expected to be present in bladder wall (Table 2B). Some of these genes were expressed in the bladder tumor samples, and probably indicate the presence of bladder wall components in these. It was striking that the single cell solutions contained much lower expression levels of these genes compared to the biopsies
10 ($p < 0.004$). Although the number of examined tumors was small this indicates that preparation of single cell solutions may reduce the presence of bladder wall cells in the samples. The absence of keratin 8 in the bladder wall sample demonstrated that this sample was devoid of urothelial cells (Table 2B).

 The genes known to be related to the bladder wall components, showed
15 a variable level throughout the samples. Some genes like myosin light chain 2 gene, fibroblast tropomyosin gene and alpha-1 collagen type IV gene, were generally more expressed in the tumor samples than the other genes (Table 2B). We hypothesize that this may reflect that there is a differential expression of genes in the connective tissue component that inevitably is included in a
20 tumor biopsy, an expression that may deviate from the one found in the bladder wall further away from the tumor. An example of this differential expression in bladder wall was the presence of transcript from the myosin light chain gene in the tumor samples but not in the bladder wall biopsies (Table 2B).

 In tumors many important events take place in the non-epithelial
25 compartment. Tumors need a connective tissue support, they need blood vessels, they interact with the immune system and have intercellular signaling with various sorts of other cells in a complicated way that has not yet been clarified in detail. Gene expression originating from the non-epithelial compartment contributes to the expression profile of a tumor, and might be of
30 great importance in relation to the clinical outcome and therapeutic response of the tumor.

EXAMPLE 3

Expression profiling of tumor pools to assess individual tumor heterogeneity.

We expected tumors from the same pathology stage and grade to have a more similar gene expression than tumors from different stages and grades. This was the case; however, these differences were not striking, and there were exceptions. Based on this we hypothesized that, a given tumor scored by a pathologist at light microscopy to be similar to another one may actually represent tumors with a remarkably different gene expression. The reason for this could be that tumors do not progress from a well defined stage to another well defined stage, but rather that a continuous change is taking place at the expression level -- which is then only partly reflected by morphology.

We tested this hypothesis by examining the expression which differed between a pool of tumors from a given stage and a single tumor, to see whether the differentially expressed genes were linked to a certain stage or whether they were a random deviation. It was evident that tumor expression that deviates from the pool systematically have expressions belonging to either a lower or a higher stage, or both, or unique expressions not seen in the pool (Fig. 3). The low stage Ta tumor had 43 genes whose expressions were increased or decreased similar to the ones seen in a Stage 2 grade IV tumor pool, and only three expressions that were altered in the opposite direction of stage 2 grade IV. The stage 2 grade IV tumor had 33 genes whose expression was either increased or decreased similar to the ones seen in the Ta superficial tumor pool, and only 8 genes altered in the opposite direction. In the T2 grade III tumor, gene expressions that were increased or decreased similar to the superficial or the grade IV invasive pool could be found. Furthermore some gene expressions were only low in this grade III tumor, and higher in both superficial and grade IV tumor pools. The clinical information on the examined single tumors (Table 3) paralleled the expression findings as the intermediate grade III tumor was the first muscle invasive tumor in a patient who had had a superficial tumor five months earlier. It seems that this tumor has not reached the level of malignancy as seen in the other invasive tumor. The latter was of

grade IV, and was a big solid tumor with muscle invasion at first visit. The superficial Ta tumor was the fifth recurrence and was followed by two new recurrences 64 and 159 days later--also of superficial nature.

5 The genes that were identified in lower stage and grade tumors and shown to be similar to the expression in high stage tumors are listed in Tables 4A and 4B. These genes may "signal" a higher stage or grade, or represent a transition from low stage or grade to high stage or grade. To aid in avoiding interpreting bladder wall expression as tumor cell-specific expression, the expression level in bladder wall is listed in Tables 4A and 4B. Two columns
10 are shown which simulate an increase in bladder wall content to 20% and 50% of the sample. These columns were obtained by adding a 20% or 50% contribution from the "bladder wall" column to the appropriate remaining percentage contribution (80% or 50%) from the TaGrII Pool column. Single tumor expression level (column labeled "Ta single tumor") was interrogated in
15 this context. Expression levels which are unlikely to be due to bladder wall contamination are shown in bold; other expressions are shown in regular font. We believe this procedure is useful and leads to reliable conclusions.

These genes form a complex group of genes with highly different functions. It is not totally unexpected that mucin synthesis is changed, nor that
20 cytokeratin 15 is decreased when moving from Ta and to higher stage. The gene expressions which signal a higher grade of atypia in already invasive grade III tumors are, among others, immunology related genes. This may indicate that the more atypical cells are either surrounded by inflammatory cells, or that the tumor cells start synthesizing these proteins. Further investigation is needed
25 to elucidate this point, and these proteins will be an interesting parameter to follow in relation to clinical course in the future. The strong up-regulation of cathepsin B may indicate an increased proteolytic attack against the connective tissue.

The cause of the changed expression is unknown and could be either
30 a transcriptional regulation or secondary to gain or loss of chromosome material. Both mechanisms are known to occur in cancer cells.

EXAMPLE 4

Change of transcript level during the progression of bladder cancer.

Biopsies from human bladder tumors were analyzed as single tumors or as pools of tumors representing the different stages in the progression of the bladder cancer disease. We used a total of 5 single tumors and 4 tumor pools, each pool made by combining six tumors. To generate a normal reference material, we pooled biopsies from normal bladder mucosa from 35 volunteers. The biopsies were disintegrated into single cell solutions immediately after removal, filtered and snap frozen in guanidinium isothiocyanate. From the cell solutions RNA was extracted, reverse transcribed to cDNA and the cDNA transcribed into labelled cRNA, that was incubated on the chip cartridges followed by scanning and scaling to a global chip intensity amounting to 150 units per probe set. The scaling made it possible to compare individual experiments to each other. To verify the reproducibility, double determinations were made in selected cases and showed a good correlation (Fig. 4A).

We compared gene expression at three different steps in the progression of bladder cancer to each other by the use of the normal pool as a reference. A scatter plot of the noninvasive pTa grade one tumor and the invasive highly abnormal grade four pT2+ tumor showed a minor subfraction of the gene transcripts to deviate much from those in the normal urothelium. The large majority of transcripts were within a narrow range in both tumors and normal urothelium (Fig. 4B,C). The number of deviating genes was higher in the most abnormal tumor.

We then analyzed transcripts that showed alterations larger than five-fold, when comparing three different pools representing the transition from normal urothelium to superficial tumor, and further on to invasive transitional cell carcinomas (TCC). The method applied consisted in a probe-to-probe comparison (20 probes per gene) based on the software GeneChip® Analysis Suite 3.1 from Affymetrix, Inc. Increased levels indicate that the transcript is either upregulated at the stated level or turned on *de novo* reaching a given fold above the background level. Decreased levels in a similar way indicate

reduction or loss of transcript. Alterations of a single transcript during the progression of the bladder cancer disease can follow several different pathways (Fig. 6). Some of the transcript changes reflect the transition from normal cells to tumor cells, and are grouped as *TCC related genes* (Fig. 6A, B). A distinct feature of group A was the presence of 6 smooth muscle related genes. Others are altered only in superficial tumors, not in invasive tumors, and are grouped as *Bladder papilloma related genes* (Fig. 6C, D). Group C, with downregulated genes, contained 15 immunology-related genes. Group D contained a variety of genes encoding proteins with different functions. Finally some genes only showed an alteration in invasive tumors and are grouped as *Invasive TCC related genes* (Fig. 6E, F). The genes in group E encoded functionally unrelated proteins, whereas group F contained 5 immunology-related genes. Thus, it seemed possible to define groups of genes whose expression level is associated with the stage of bladder tumors.

EXAMPLE 5

Cluster Analysis

The level of a gene transcript during disease progression can be thought of as a pattern that can be correlated to patterns of other gene transcripts. If the expression of one gene is very similar to the expression of another gene in several samples they are a correlated pair of genes. This pair of genes can then be correlated to other genes with a similar transcriptional behavior in the set of tissues examined, and together these constitute a gene cluster. In the next step the relation between clusters is established and a dendrogram of genes is formed, in which strongly correlating gene clusters are near each other. The principles are described in Eisen et al., Proc. Natl. Acad. Sci. USA 95, 14863 (1998). Briefly, each gene vector was placed in its own cluster, where the cluster prototype was set to the gene vector. All pair-wise vector angles between cluster prototypes were calculated. The smallest vector angle was identified, and those clusters were merged as a weighted average of the two prototypes (and also a weighted average of all the gene vectors each prototype represented). The vector angles were then updated between the newly merged

clusters and the merger process was repeated. The final clusters are displayed in the order in which they were merged.

Exactly the same procedure used to cluster genes can be used to cluster the tissue samples, showing the relation between the different tissues based on their gene expression. We based clustering analysis on either the 4067 transcripts being scored as present in at least one of the samples, or based on those 400 transcripts (see Table 9) that covaried best with a weighting scheme adding increasing values to increasing stages.

The scaled AvgDif measures as calculated by the Affymetrix software were extracted for the normal pool and each of the graded tissues. Only the 4067 genes with an AbsCall of P (present) in at least one of the tissues were considered. All AvgDif measures below 20 were set to 20. For each tissue and each gene, the AvgDif from the normal pool was either subtracted, to define the "absolute difference," or divided and natural logarithm applied to define the "log-fold" relative measure. The relative expression measures for each tissue (log-fold or absolute difference) were used to cluster tissues by a hierarchical method using the Euclidean distance between tissues. Tissue dendrograms were constructed with the PHYLIP program using clustering order and distances. A weighting scheme (see Example 6) for the seven observed stages and grades of cancer was used to select 200 positively covarying and 200 negatively covarying genes with respect to progression. The same hierarchical method and a normalized Euclidean distance (vector angle) were used to cluster the top 400 positively and negatively covarying genes for both relative expression measures. Gene dendrograms were constructed by the same method as for the tissue dendrograms.

Tissue clusters

Different algorithms based on either fold change or absolute differences in transcript levels across the different samples were applied to all transcripts or only those covarying with a progression scale. Both methods were able to cluster the tissues according to the tumor's or tumor pools stage and grade of atypia in a meaningful way (Fig. 5). The two noninvasive and the two invasive

pools each clustered very closely together both using the fold change and the absolute difference, indicating a close genetic relation between these, and indicating that one effect of pooling samples is a reduction of the variation in gene expression. The single tumor preparations showed a more varied
5 distribution but still reflected the stage of the tumor. In the log-fold dendrograms (Fig. 5A, C) the superficial tumors 335, 837 and 901 cluster close to the superficial pools, but the pTa grade III tumor 901 seems closer to the superficial pools than the pTa grade II tumor 837. This may either be due to the variation in histopathological grading or due to the tumors having different
10 genetic properties. The minimally invasive pT1 grade III tumor 320 is correctly placed in between the muscle invasive and the superficial tumors, and the muscle invasive tumor 713 is placed very close to the pools of pT2+ tumors. Tumor 713 seemed to be closer to the pT2+grade IV than Grade III pool although it was histopathologically scored as grade III. In the absolute
15 difference dendrogram (Fig. 5B, D) the superficial tumors 837 and 901 are closely related to the superficial pools, the pT1 superficially invasive tumor is less related and finally the invasive tumor 713 located closest to the invasive pools. An exception was the superficial tumor pTa grade I, 335-6 that deviated from all other tumors. Whether this tumor has unique properties is unknown,
20 however it did not deviate from the expected location in the dendrograms based on fold change.

The dendrograms show that the clustering algorithms work very well, that the dataset obtained from the oligonucleotide arrays reflect the biological properties of the tumors, and that objective information on a tumor's stage and
25 grade can be obtained from mathematical analysis of gene expression data. Furthermore, it is seen that when ranking based on covariance to the progression is used to extract the top 10% covarying genes, these have a dendrogram that is almost identical to the one based on 4067 genes. We therefore used the ranking procedure when analyzing gene clusters.

Gene clusters

The data obtained from cluster analysis are presented as colored images in which genes with similar expression patterns are clustered next to each other on the vertical axis and the samples according to stage and grade on the horizontal axis (Fig. 7). The color of each cell in the tabular image represents the ratio between the sample expression of the gene in question and the expression in normal urothelium. The color saturation is directly proportional to the magnitude of the measured expression ratio, cyan indicating the lowest ratio, yellow indicating the highest ratio. Black indicates a ratio of one, a similar level of expression in tumor as in normal urothelium. The two different clustering methods, log-fold and absolute difference gave completely different clusters across the set of samples (Fig. 7).

In the log-fold based cluster analysis, the top 200 positively covarying genes can be divided into five different clusters containing functionally related genes (Fig. 7, left upper column). The cluster shown at the top contains genes related to cell proliferation such as cyclins A and E, PCTAIRE-1, and SWI/SNF. The next cluster mainly contains oncogenes and growth factors. Genes in both these clusters are expressed at a level close to that seen in normal urothelium in superficial tumors (black) and increase during disease progression (yellow). The two clusters at the lower part show a reduced expression level in the superficial tumors compared to normal (cyan) and then an increase above the normal urothelial level in invasive tumors (shades of yellow). These clusters contain a set of immunologically related genes, like different MHC's and immunoglobulins, cancer related genes like src-like kinase and Fas/Apo-1, and finally another immunologically related cluster at the bottom.

The 200 negatively covarying genes (Fig. 7, left lower column) could be divided into three different clusters based on log-fold change and function of the genes. The upper cluster contains genes related to cell adhesion like laminins, integrins and P-cadherin (Fig. 7, left lower column). They all show a reduced level of expression in the invasive tumors as evidenced by the cyan

coloring to the right. The small middle cluster contains four genes related to transcription, and finally the lowest cluster in the figure contains five proteinases, like cathepsin E (two different probe sets for the same gene) and metalloproteinase as well as a protease inhibitor. The lower clusters are characterized by an increase in level in superficial tumors (yellow) followed by a reduction to a level below normal urothelium in invasive tumors.

In the absolute difference based cluster analysis the top 200 covarying genes that showed a positive covariance contained only few clusters having a functional relation. The upper cluster (Fig. 7, right upper column) contained five genes related to cell proliferation like the microtubule-associated protein and oncoprotein 18/stathmin. The next cluster was a set of immunology related genes like MHC and LERK-2. Both these clusters showed an increased expression level in invasive tumors compared to normal urothelium. The cluster at the lower end of the figure showed a reduced level in superficial tumors and a return to normal or increased level in invasive tumors. This cluster contained many immunology-related genes like MHC, HLA and immunoglobulin genes. Finally, for genes that showed a negative covariance based on absolute difference (Fig. 7, right lower column), this was mainly due to clustering of ribosomal genes. A very tight cluster in the middle of the graph show ribosomes that are upregulated in expression in superficial tumors and downregulated or unaltered in invasive tumors. The middle ribosomal cluster is generally expressed at a lower level than in normal urothelium, whereas the cluster at the bottom of the figure is similar to the one in the middle. Other genes that seemed to cluster were a small tight cluster of immunology related genes, and two tumor inhibitors, TGF-beta superfamily protein and Sui1 in the uppermost cluster.

Thus, a pattern of altered gene transcription occurs during the progression of bladder cancer that involves a number of genes belonging to functionally different gene families. Cluster analysis identified many biologically relevant genes, and in that aspect was superior to the probe-by-probe comparison described above.

MISSING AT THE TIME OF PUBLICATION

where
$$dp(X,Y) = \sum_{i=1}^n (x_i \times y_i)$$

and
$$len(X) = \sqrt{\sum_{i=1}^n x_i^2}$$

After the sample had been compared in this way to each pool, invasive and non-invasive, the pool which differed from the sample by the smaller angle was determined to be the class of the sample.

Samples from ten bladder tumors were assigned by the classifier, and the results are shown in Fig. 8. The classifier was able to correctly call the presence or absence of muscle invasion in all ten samples examined (7 non-muscle invasive, 3 muscle invasive), based on categorizations made by a pathologist. To cross-validate the classification methodology, two non-invasive (Ta) and two invasive (T2) pools were compared with tumors from each of 10 patients. Since two pools were available for each stage, four possible combinations (classifier sets) of one Ta pool and one T2 pool were tested. The classification rate was calculated as the number of tumors correctly identified times 10. The results for each of the four classifier sets were averaged to obtain the data shown in Fig. 8.

EXAMPLE 7

Confirmation of microarray expression analysis by Northern blotting

In order to confirm the array data, Northern blotting was performed on the same samples of RNA as used for array hybridization. A standardized amount of RNA was run in each lane, followed by blotting with a labelled RNA probe, and quantitation of the band obtained (Fig. 9).

Total RNA, 0.5–4 µg per lane, was separated in 1.5% agarose-formaldehyde gels, transferred onto Zeta-Probe® nylon membrane (Bio-Rad) by positive pressure (Posiblotter, Stratagene) and immobilized by baking for 20 min at 120°C. The filters were hybridized with digoxigenin-labelled (DIG) RNA transcribed from 600-1000 bp PCR products containing a T7 promotor

incorporated via the antisense primers. Filters were hybridized with 10 ng probe per ml of ultrahyb™ hybridisations solution at 68°C for 16 h and washed to a stringency of 0.1x SSC at 68°C. Specific hybridization was detected by reacting the membrane with monoclonal anti-DIG antibodies conjugated with alkaline phosphatase, incubating with ECF chemifluorescence substrate (AmershamPharmacia) and scanning on a Storm 840 (Molecular Dynamics). The hybridization signals were quantified with ImageQuant 5.0 software.

As can be seen from the plots, the oligonucleotide array and the Northern blot gave similar results with the different probes, both in genes expressed at a high level (beta2-microglobulin), and those expressed at a very low level (CD59).

EXAMPLE 8

Immunohistochemical localization of expressed proteins

The biopsy samples used to study gene expression in bladder tumors contain cells other than urothelial cells, although the amount of other cells should be limited due to the use of single cell solutions. We therefore used immunostaining of tissue sections from the single tumors examined to determine which cells expressed the protein encoded by the transcript in question. We used the transcript levels to select a group of proteins supposed to show variation from sample to sample, making possible a rough correlation between level of protein detected and intensity of the transcript on the microarray.

Four µm sections were cut from paraffin-embedded tissue blocks, mounted, and deparaffinized by incubation at 80°C for 10 min, followed by immersion in heated oil at 60°C for 10 min (Estisol 312, Estichem A/S, Denmark) and rehydration. Antigen retrieval was achieved in TEG (Tris-EDTA-Glycerol) buffer using microwaves at 900 W. The tissue sections cooled in the buffer for 15 min before a brief rinse in tap water. Endogenous peroxidase activity was blocked by incubating the sections with 1% H₂O₂ for 20 min, followed by three rinses in tap water, 1 min each. The sections were then soaked in PBS buffer for 2 min. The next steps were modified from the

descriptions given by Oncogene Science Inc., in the Mouse Immunohistochemistry Detection System, XHCO1 (UniTect, Uniondale, NY, USA). Briefly, the tissue sections were incubated overnight at 4°C with primary antibody (against beta-2 microglobulin (Dako), cytokeratin 8, cystatin-C (both from Europa, US), junB, CD59, E-cadherin, apo-E, cathepsin E, vimentin, IGFII (all from Santa Cruz), followed by three rinses in PBS buffer for 5 min each. Afterwards, the sections were incubated with biotinylated secondary antibody for 30 min, rinsed three times with PBS buffer and subsequently incubated with ABC (avidin-biotinylated horseradish peroxidase complex) for 30 min, followed by three rinses in PBS buffer. Staining was performed by incubation with AEC (3-amino-ethylcarbazole) for 10 min. The tissue sections were counter stained with Mayers hematoxylin, washed in tap water for 5 min. and mounted with glycerol-gelatin. Positive and negative controls were included in each staining round with all antibodies.

We found several of the proteins to be expressed not only by urothelial cells but also by leukocytes, endothelial cells or histiocytes (Table 10, Fig. 10). Of the examined proteins only keratin 8 and ApoE were confined to urothelium; the other proteins were also present in other cell types. Based on the assumption that transcript and protein originates from the same cell, this clearly indicates that conclusions on the origin of the transcripts requires a histological examination, or other verification procedure. The amount of stroma in a biopsy, the vascularization (amount of endothelial cells), the level of leukocyte infiltration, and the grade of atypia of the urothelial cells were all parameters that seemed to influence the level of a given transcript.

The level of protein identified by immunostaining, disregarding the cell type expressing the protein, correlated well with the transcript level measured on the microarray (Fig. 10). However, no attempt was made to quantitate the immunostaining due to the often large heterogeneity in staining across the sections.

Table 1

Gene name	Description	Con tissue	BT33-2	BT33-1	BT33-1
		Bladder Wall	T ₁ q _{III}	T ₂ q _{III}	T ₂ q _{IV}
Structural proteins					
X00449.1	Human cytochrome b5 gene, complete cds	4208	26	78	87
X07695.1	Human mRNA for cytochrome b5 C-terminal region	7458	27	78	87
L42601.1	Human keratin 5 isoform K5c (KRT5C) gene	5155	183	128	389
L42582.1	Human keratin 6 isoform K6a (KRT6A) gene	4939	125	155	388
V01519.1	Human messenger RNA encoding cytoskeletal keratin (type II) mRNA from cultured epidermal cells	4779	140	175	364
X00351.1	Human mRNA for beta-actin	4188	2879	1189	1322
M10277.1	Human cytoplasmic beta-actin "gene," complete cds	3788	3321	3788	1830
H02815-HT4023.1	"Myosin," Light "Chain," "Atrial," Smooth Muscle "(G0:U02829)," Smooth "Muscle," "All Splice"	3415	3458	4176	2003
H02815-HT4023.1	"Myosin," Light "Chain," "Atrial," Smooth Muscle "(G0:U02829)," "Non-Muscle," "All Splice 2"	2285	3887	4148	2018
X57683.1	Human mRNA for keratin 4 (K4) (X07683) type-RNA	2126	125	160	193
L42611.1	Human keratin 6 isoform K6c (KRT6C) "mRNA," complete cds	1946	301	228	224
H02815-HT4023.1	"Myosin," Light "Chain," "Atrial," Smooth Muscle "(G0:U02829)," "Non-Muscle," "All Splice 2"	1926	1594	2811	1178
M05787.1	Human 22kDa smooth muscle protein (SM22) "mRNA," complete cds	1735	68	318	2328
M55898.1	Human alpha-1 collagen type I "gene," "3' end"	1610	423	4218	1874
M21589.1	Human keratin type II (58 kD) "mRNA," complete cds	1572	20	20	811
X15839.1	Human mRNA for vesicular smooth muscle alpha-actin	1405	20	329	1164
Metabolic, catalytic, and anabolic enzymes					
U46922.1	Human cystathionine B gene, complete cds	10070	859	483	1687
X01877.1	Human liver mRNA for glyceraldehyde-3-phosphate dehydrogenase "(G3PD," EC 1.2.1.12)"	3234	3018	3048	1064
D78381.1	Human mRNA for ornithine decarboxylase "antizyme," ORF 1 and ORF 2	2518	2181	2373	4422
U99099.1	Human ubiquitin gene, complete cds	2053	2902	2821	3237
M96400.1	Human phospholipase A2 "mRNA," complete cds	1553	1320	1048	1051
M34483.1	Human sapiens (clone pGIST-01) glutathione S-transferase pi (GSTP1) "gene," complete cds	1522	2457	1493	544
M25860.1	Human ubiquitin "mRNA," complete cds	1506	599	908	1072
M63178.1	Human cathepsin D (catD) gene	1489	695	1131	1990
X77584.1	Human mRNA for ATL-derived factor/retrocin	1470	815	713	568
X02152.1	Human mRNA for lactate dehydrogenase-A "(LDHA," EC 1.1.1.27)	1432	1478	491	1173
M27897.1	Human cystatin C (CST3) gene	1363	1026	730	2233
X58997.1	Human UbA52 gene coding for ubiquitin-52 amino acid fusion protein.	1358	1414	1298	1637
Proteins related to transcription and translation					
Z12982.1	Human mRNA for homologous to yeast ribosomal protein L41	7488	8785	8449	8798
X59150.1	LOC432 Human mRNA for ribosomal protein S18	5256	6302	4994	2859
L06499.1	Human sapiens ribosomal protein L37a (RPL37A) "mRNA," complete cds	5054	6841	6648	4138
L04483.1	"Human ribosomal protein S21 (RPS21) "mRNA," complete cds"	5832	10817	9062	2848
X02680.1	Human mRNA for ribosomal "protein," complete cds	5345	4337	4331	5096
J04817.1	Human elongation factor EF-1-alpha "gene," complete cds	4935	8865	7517	2180
X17208.1	Human mRNA for LURap3	4828	8042	8931	4029
U14969.1	Human ribosomal protein L28 "mRNA," complete cds	4539	4958	3427	4979
M68854.1	Human ribosomal protein S16 "mRNA," complete cds	4473	5801	5019	4247
H02873-HT3017.1	Ribosomal Protein L30 Homolog	4372	8812	7949	4102
M81757.1	Human S19 ribosomal protein "mRNA," complete cds	4369	8727	4087	4311
U14973.1	Human ribosomal protein S29 "mRNA," complete cds	4281	5175	4134	4410
H03366-HT3541.1	Ribosomal Protein L37	4242	7295	4338	3574
X03659.1	Human mRNA fragment for elongation factor TU (A-terminus), (p=K03659) type-RNA	4233	8855	4181	1506
X03659.1	Human mRNA for 23 kD highly basic protein	4210	6481	5730	5089
X03659.1	Human mRNA for ORF	3963	4047	3534	3591
U14970.1	Human ribosomal protein S5 "mRNA," complete cds	3928	4473	2410	2589
U14968.1	Human ribosomal protein L27a "mRNA," complete cds	3885	3772	3079	4104
X03342.1	Human mRNA for ribosomal protein L32	3818	5824	4184	3384
X07247.1	Human sapiens p58 gene for ribosomal protein S8	3725	3928	2702	3165
U14972.1	Human ribosomal protein S10 "mRNA," complete cds	3695	6292	2394	2903
M17885.1	Human acidic ribosomal phosphoprotein P0 "mRNA," complete cds	3680	4911	4728	5335
H01850-HT1823.1	Ribosomal Protein S20	3582	3589	3893	4271
M17886.1	Human acidic ribosomal phosphoprotein P1 "mRNA," complete cds	3488	3038	3138	2648
X05617.1	Human mRNA for ribosomal protein S11	3387	4561	4705	3744
U15940.1	Human mRNA for ribosomal protein L31	3375	8960	5371	3528
U12465.1	Human ribosomal protein L33 "mRNA," complete cds	3327	5875	2108	3004
M18000.1	Human ribosomal protein S17 "gene," complete cds	3315	6115	4537	2410
X05527.1	Human mRNA for ribosomal protein L19	3282	5745	4830	1832
M13934.1	Human ribosomal protein S14 gene, complete cds	3281	3512	1927	2578
M04718.1	Human ribosomal protein S25 "mRNA," complete cds	3228	2827	2087	3181
U14199.1	"Human laminin receptor (2H8 epitope) "mRNA," "3' end"	3222	8316	8902	1812
L06505.1	Human ribosomal protein L12 "mRNA," complete cds	3074	4581	3541	2787
X73480.1	Human mRNA for ribosomal protein L3	2949	2230	1849	2458
X02691.1	Human mRNA for ribosomal protein (homologous to yeast S24)	2985	3540	3732	1534
U14971.1	Human ribosomal protein S9 "mRNA," complete cds	2545	1807	1361	2503
M77232.1	Human ribosomal protein S6 gene, complete cds and flanking regions	2518	1948	1982	2470
X79234.1	Human mRNA for ribosomal protein L11	2502	2298	2184	2290
U09953.1	Human ribosomal protein L9 "mRNA," complete cds	2506	2840	2851	1911
X53954.1	Human mRNA for H23 ribosomal protein homolog	2495	5371	3501	2851
Z08876.1	Human sapiens gene for ribosomal protein L38	2490	4036	2418	2159
M32053.1	Human H19 RNA "gene," complete cds (spliced in vivo)	2486	8187	2845	320
L38941.1	Human sapiens ribosomal protein L34 (RPL34) "mRNA," complete cds	2480	4228	2950	2034
Z08407.1	Human sapiens mRNA for ribosomal protein L8	2386	2775	1342	1797
Z49148.1	Human sapiens mRNA for ribosomal protein L29	2303	4080	2201	1028
X04707.1	Human sapiens BSC1 mRNA	2268	3402	2224	2230
M31520.1	Human ribosomal protein S24 mRNA	2242	9267	4925	1409
D14530.1	Human homolog of yeast ribosomal protein "S20," complete cds	2193	2112	1881	945
H0821-HT821.1	Ribosomal Protein S13	2158	1867	1440	1700
M08074.1	"Human ribosomal protein L7a (surf 3) large subunit "mRNA," complete cds"	2150	8188	2380	1000
U58882.1	Human ribosomal protein S28 "mRNA," complete cds	2129	3034	1978	1929
X09491.1	Human mRNA for ribosomal protein L5	2094	2796	2790	1187
H033-HT33.1	Ribosomal protein S4	2077	1656	1078	1277
A0001533.1	Human mRNA for "Dol," complete cds	2083	2155	1707	217
M55408.1	"Human pancreatic tumor-related protein "mRNA," "3' end"	1932	4150	1819	815
L19527.1	Human sapiens ribosomal protein L27 (RPL27) "mRNA," complete cds	1931	3103	2241	2052
H04319-HT4589.1	Ribosomal Protein L5	1900	2281	1600	1370
X53777.1	Human L23 mRNA for putative ribosomal protein	1915	3100	2330	1075
M31520.1	Human ribosomal protein S24 mRNA	1876	2419	2367	1416
H0613-HT613.1	Ribosomal Protein S12	1873	2156	2000	1145
X56715.1	Human Huma3 mRNA for 40S ribosomal protein s3	1744	2569	2106	843
D79209.1	Human mRNA for ribosomal protein "L32," complete cds	1833	2212	1743	1566
X51345.1	Human jun-B mRNA for JUN-B protein	1445	150	330	721
D87735.1	Human mRNA for ribosomal protein "L14," complete cds	1439	1999	1506	1308
X57959.1	Human mRNA for ribosomal protein-L7	1425	1789	1880	508
H0244-HT384.1	Ribosomal Protein L26	1409	2438	1347	1111
L11509.1	Human sapiens ribosomal protein L18 (RPL18) "mRNA," complete cds	1399	1878	1204	1144
H04547-HT4967.1	Ribosomal Protein L10	1378	3325	1728	1556
L28247.1	Human sapiens subunit 1 "mRNA," complete cds	1375	1812	1521	1099
X52866.1	Human mRNA for ribosomal protein L35a	1361	1280	910	1415

Proteins involved in posttranslational modification		9609	20	939	5099
Z23090_at	H sapiens mRNA for 28 kDa heat shock protein	1161	9689	5541	2883
S78522_at	Jarid3in carboxyl extension protein [human," mRNA," 560 nt]	2522	2390	1894	1684
U12404_at	Human Csa-19 "mRNA," complete cds	377	71	165	343
X54277_at	H sapiens CL 100 mRNA for protein tyrosine phosphatase	1727	1798	2284	1278
X52851_ma1_at	Human cyclophilin gene for cyclophilin [EC 5.2.1.8]				
Cell membrane proteins		2387	1058	1191	2583
DD0017_at	Human lipocalin II mRNA	1423	1013	1244	1902
M33880_at	Human 26-kDa cell surface protein TAPA-1 "mRNA," complete cds				
Secreted proteins/hormones/growth factor related proteins		2774	3792	4130	8117
M17733_at	Human thymosin beta-4 "mRNA," complete cds				
Proteins related to immunology		4579	20	5638	9005
M83439_s_at	"Human Ig rearranged gamma chain "mRNA," V-J-C region and complete cds"	3684	2784	6031	2841
J00105_s_at	"Human beta-2 microglobulin gene "mRNA," 3' end"	3447	20	3373	11585
M57789_s_at	"Human (hybridoma H210) anti-hepatitis A IgG variable "region," constant "region," complementant	3378	2880	1904	2591
M24194_at	Human MHC protein homologous to chicken B complete protein "mRNA," complete cds	2821	1098	1449	2367
D46824_s_at	Human HLA-B null allele mRNA	2780	429	2264	3208
X00274_at	Human gene for HLA-DR alpha heavy chain class II antigen (immune response gene) of the major	2360	1125	3442	3978
S82287_at	"beta 2-microglobulin (111b deleted between nucleotides 98-99) "human," colon cancer cell line "H	2235	137	1422	9736
M34516_at	Human omega 3 light chain protein 14.1 (Ig lambda chain related) gene	1875	20	145	544
M34529_at	Human adipsin/complement factor D "mRNA," complete cds	1473	54	723	4064
S71043_ma1_s_at	Ig alpha 2-immunoglobulin A heavy chain subtype 2 (constant "region," germ line) "human," peripheral	1449	1184	1215	1058
M57710_at	Human IgE-binding protein (epsilon-BP) "mRNA," complete cds				
Nucleoproteins		3851	3351	2542	3234
M84711_at	Human v-fos transformation effector protein (Fos-1) "mRNA," complete cds	2812	8360	9363	1838
U42801_ma1_s_at	Human J7 HD laminin receptor precursor/p40 ribosome associated protein "gene," complete cds	2851	4333	5077	1310
D13413_ma1_s_at	Human mRNA for tumor-associated 120 kDa nuclear protein "p120," partial cds(carboxyl terminus)	2005	1873	1418	2290
D32405_at	Human homolog of rat insulinoma gene (pig)," exon 6-Jin	1697	1853	3281	1581
M11353_at	Human H3.3 histone class C "mRNA," complete cds	1448	1117	1338	1175
M28813_at	Human nucleophosmin "mRNA," complete cds	1438	1139	1225	1493
J03827_at	Y box binding protein-1 (YB-1) mRNA				
Mitochondrial proteins		7848	3970	5895	5823
Z70759_at	H sapiens mitochondrial 16S rRNA gene (partial, 190-270759 nt) type=RNA	1338	1580	1649	1405
X15341_at	Human COX VIa-L mRNA for cytochrome c oxidase liver-specific subunit VIa (EC 1.9.3.1)				
Other proteins		15733	1713	381	1298
M28311_s_at	Human cystic fibrosis antigen mRNA, complete cds	10368	20	20	20
M8757_s_at	S100 Calcium binding protein A7	5344	64	104	162
L05187_at	"Human septins small protein-rich protein 1 (SPRR1A) "gene," complete cds"	5388	20	39	310
L10343_at	Human elastin "gene," complete cds	3167	52	114	171
D88422_at	Human DHA for cystatin A	4856	8358	4730	3894
HG3214-HT3391_at	Metalloproteinase 1	4930	20	20	319
M71006_at	Human migration inhibitory factor-related protein 8 (MIRP8) "gene," complete cds	4572	3638	3890	3168
X18084_at	Human mRNA for transcriptionally controlled tumor protein	4485	59	20	20
L05188_at	"Human septins small protein-rich protein 2 (SPRR2B) "gene," complete cds"	4441	20	20	20
M18888_at	"Human small protein rich protein (Aprt) "mRNA," clone 128"	4285	117	33	40
X53065_f_at	Human SPR2-1 gene for small protein rich protein (exon 2)	3885	3603	2730	1274
X58482_f_at	H sapiens TNNT2 gene exon 11 (19ntX58482 nt) type=DNA format=mRNA	3843	3170	2728	4056
HG3549-HT3751_at	Wilm's Tumor-Related Protein	3809	20	28	20
M20030_f_at	"Human small protein rich protein (Aprt) "mRNA," clone B30"	3490	20	20	20
X78223_s_at	H sapiens MAL gene exon 1 (and joined CDS).	3217	182	283	333
X06908_at	Human mRNA for lipocalin	3172	7843	8178	4858
M11147_at	Human ferritin L chain "mRNA," complete cds	3031	20	52	384
M57348_s_at	H sapiens mRNA (clone 9712)	2805	1553	1408	2416
V05594_s_at	Human mRNA for metallothionein from cadmium-treated cells	2575	7538	6245	1892
U08155_s_at	Human chromosome 1q subclonal sequence O15553, 19ntX08155 nt) type=DNA format=CDS	2525	186	378	332
U54856_at	Human fatty acid binding protein homologue (FA-FABP) "mRNA," complete cds	2378	27	47	2971
Y07758_at	H sapiens S100A2 "gene," exon "1," 2 and 3	2156	3154	2439	1379
U78027_ma3_at	Human septins Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-lyc ribosomal pro	2101	1427	1223	1336
D38853_at	Human mRNA for "calpainin," complete cds	1945	1342	2580	2832
X57351_s_at	Human 1-50 gene from interferon-inducible gene family	1819	2870	1179	825
M38581_at	Human septins cellular ligand of annexin II (p11) "mRNA," complete cds	1771	2131	1619	1776
L20941_at	Human ferritin heavy chain "mRNA," complete cds	1655	123	245	548
M57813_at	Human retinol acid-binding protein II (CRABP-II) gene	1652	79	66	62
X53296_s_at	H sapiens mRNA for IRAP	1525	20	20	451
X04470_s_at	Human mRNA for embryokoprosin (ALP) from cervix uterus	1472	1380	1439	1450
M57951_at	H sapiens mRNA for proliferation-associated gene (pag)	1416	213	360	149
HG4089-HT4339_s_at	Monocyte Chemoattractant Protein 1	1399	21	28	50
V07808_at	H sapiens mRNA for Progression Associated Protein	1311	323	557	911
J04152_ma1_s_at	M181 gene isolated from Human gastrin-releasing tumor-associated antigen GA733.1 protein "gene,"	1310	188	190	202
S81914_at	(EX-1) expression-inducible immediate-early gene "human," "intronic," mRNA "Partial," 1223 nt)				

Bladder wall compared to single cell solutions and biopsies of tumors

Gene name	Gene product	Biopsy Bladder wall	Single cell solutions				Biopsies			
			Ta	Grl	Ta	Grl	T1	Grl	T2	Grl
L05188_f_at	Human sapiens small proline-rich protein 2 (SPRR2B) "gene," complete cds	4465	-	-	-	-	-	-	-	310
L10343_at	Human elafin "gene," complete cds	5388	-	-	-	-	-	-	-	386
L42583_f_at	Human sapiens keratin 6 isoform K6a (KRT6A) gene	4939	384	348	-	-	425	389	-	389
L42601_f_at	Human sapiens keratin 6 isoform K6c (KRT6C) gene	5155	475	391	-	-	544	-	-	-
M19888_at	Human sapiens small proline rich protein (sprl) "mRNA," clone 128	4441	-	-	-	-	-	-	-	319
M2030_f_at	Human small proline rich protein (sprl) "mRNA," clone 930	3809	-	-	-	-	-	-	-	611
M21005_at	Human migration inhibitory factor-related protein 8 (MRP8) "gene," complete cds	4830	-	-	-	-	-	-	-	-
M21389_at	Human migration inhibitory factor-related protein 8 (MRP8) "gene," complete cds	1572	-	-	-	-	-	188	-	516
S61914_at	Human keratin type II (58 kD) "mRNA," complete cds	1310	-	-	-	-	-	-	-	-
V01516_f_at	Human keratin type II (58 kD) "mRNA," complete cds	4779	452	300	-	346	478	-	78	-
X07695_at	Human messenger fragment encoding cytoskeletal keratin (type II)	7458	-	-	-	-	-	-	-	-
X53085_f_at	Human SPR2-1 gene for small proline rich protein (exon 2)	4285	-	-	-	178	-	-	-	193
X67683_at	Human SPR2-1 gene for small proline rich protein (exon 2)	2126	-	223	-	-	154	126	160	343
X68277_at	Human sapiens mRNA for keratin 4 (kb-X67683) "type-RNA"	1972	87	78	-	81	119	71	165	71
Y07909_at	Human sapiens CL 100 mRNA for protein tyrosine phosphatase	1399	-	76	-	-	114	-	-	-
	Human sapiens mRNA for Progression Associated Protein									

Table 2A

Expression of genes related to bladder wall

Gene name	Gene product	Bladder wall	Single cell solutions					Biopsies				
			Ta Gr1	Ta Gr1	Ta Gr1	T1 Gr1	T2 Gr1	Mean	T1 Gr1	T2 Gr1	T2 Gr1	Mean
Z19554_s_at	H.sapiens vimentin gene	1186	-	-	-	422	204	125	334	853	674	620
J02854_at	Human 20-kDa myosin light chain (MLC-2)	412	-	-	-	-	-	0	-	-	615	205
M21812_at	Human (clone PWHLC2-24) myosin light chain 2	175	-	433	-	-	690	225	374	427	410	404
U48959_at	Human myosin light chain kinase (MLCK)	621	-	-	-	-	-	-	-	-	617	206
X05276_at	Human mRNA for fibroblast tropomyosin TM30 (pI)	642	261	313	294	245	139	250	178	283	214	225
Z24727_at	H.sapiens tropomyosin isoform	464	55	76	98	56	59	69	365	468	607	480
M12125_at	"Human fibroblast muscle-type tropomyosin "	586	-	-	-	-	-	0	-	-	426	142
M19267_s_at	"Human tropomyosin "	284	-	90	-	207	-	59	482	313	188	334
M63391_rna1_at	Human desmin gene, complete cds.	392	-	192	-	-	-	38	-	-	905	302
M26576_cds2_at	Human alpha-1 collagen type IV gene, exon 52.	207	-	-	-	-	-	0	-	-	290	97
Sum of expressed units		4869	316	1104	392	930	1092	767	1743	2344	4956	3014
X74929_s_at	H.sapiens KRT8 mRNA for keratin 8	5006	2266	3494	2434	2450	3130	2074	1423	390	1296	

Table 2B

Table 3. Number of genes, out of 3400 genes examined, that are expressed as in the tumor-pool to which the tumor belongs, or altered as in a tumor pool of higher or lower stage or grade

Clinical data on tumor	5th superficial recurrence Grade II	First invasive tumor Grade III	Primary tumor, large solid muscle invasive Grade IV
Expression like tumor pool	770 genes	516 genes	625 genes
Unique to tumor	58	75	93
Increased expression similar to invasive Grade IV pool	24	47	-
Decreased expression similar to invasive Grade IV pool	19	22	-
Increased or decreased similar to Grade II		45	33

The lines in bold list genes that signal a higher stage or grade.

Table 4A
Gene expression that signal a higher grade or stage

Gene Name	Gene product	Ts-01 Pool	Ta Single Tumor	T201V Pool	Deviation*	Bladder wall	20% Wall**	50% Wall
HQ3147-4T2217r_at	Mucin "3," intestinal (Gc:1669406)	0	330	541	On	0	0	0
HQ860-4T1880_at	Human mucin 6, gastric (single repeat clone)-human (fragment), partial CDS	0	426	493	On	0	0	0
Y00707_s_at	Human mRNA for MDMP (monocyte-derived neutrophil chemotactic factor)	0	327	393	On	224	44.9	112
B021300_f_at	Human unproductively rearranged Ig mu-chain mRNA V-region (VD), 8' end, clone mu-3A1A	0	284	219	On	0	0	0
X83462_at	Human mRNA for Fas/Apo-1 (clone pCRTM11-Fasdelta[4,7])	0	236	367	On	0	0	0
X07690_at	Human mRNA for cytochrome 1b	323	0	0	Off	0	262.4	164
J06030_s_at	Human cathepsin E "mRNA," complete cds	1145	302	0	Decreased	0	916	872.6
B04424_at	Human cathepsin E (CTSE) gene	413	0	0	Decreased	0	330.4	206.6
U20794_s_at	Human transcription factor JunB [JunB] "gene," 5' region and complete cds	1250	324	0	Decreased	1060	1213.8	1169.5
X59768_at	Human PRAD1 mRNA for cyclin	438	0	0	Off	63	381.4	249.5
L35293_at	Human Cdc25 binding protein (CDBP1) "mRNA," complete cds	162	0	0	Off	0	129.6	61
B17083_s_at	Human prepro-neutrophil-like growth factor II (ILF-II) variant "mRNA," complete cds	1683	489	0	Decreased	0	1339.4	831.5
B062403_s_at	Human insulin-like growth factor binding protein 4 (IGFBP4) "mRNA," complete cds	998	245	0	Decreased	337	841.8	652.5
M34370_s_at	Homo sapiens (clone lambda MSP131) beta-microglobulin protein (MSP) gene	260	0	0	Off	0	224	140
U22170_s_at	Human prolactin secretory protein 57 "mRNA," complete cds. Ap-4U22178 polyA+RNA	69	0	0	Off	0	71.2	44.5
U69263_at	Human matrilin-2 precursor "mRNA," partial cds	116	0	0	Off	152	123.2	134
U72649_at	Human BTG2 (BTG2) "mRNA," complete cds	886	274	289	Decreased	244	787.8	666
U81008_at	Human p76 "mRNA," complete cds	183	0	0	Off	76	168.6	134.5
U93816_at	Human clone 23815 mRNA sequence	250	0	0	Off	31	206.2	140.5
X63576_fna1_at	H sapiens gene for parvalbumin	176	0	0	Off	0	140.8	68
X76180_at	H sapiens mRNA for lung anion chloride sensitive Na+ channel protein	263	0	0	Off	255	253.4	254
X07159_at	H sapiens mRNA for beta subunit of epithelial anion chloride-sensitive sodium channel	188	0	0	Off	0	150.4	94
Y00264_at	Human mRNA for amyloid AA precursor of Alzheimer's disease	236	0	0	Off	183	272.8	238
Z76693_s_at	H sapiens mRNA for protein-tyrosine phosphatase NC-PTP/COM1	195	0	0	Off	0	156.8	98

Only genes scored as present are shown. *Deviation describes aberration from pool = 20% and 50% describes expected units of expression if tumor pool was added 20% or 50% bladder wall components. Genes in bold do not need interrogation of bladder wall contribution. Off, genes that are turned off; On, genes that are turned on.

Table 4B Gene expression that signal a higher grade or stage

Gene Name	Gene Product	T2GIII Pool	2GIII Single turn	T2GIV Pool	Grade III po	Grader wall	20% Wt%	60% Wt%
X73501_at	Human gene for cytokinin 20	0	162	102	On	0	0	0
X03689_s_at	Human mRNA fragment for elongation factor TU (N-terminal)	0	1845	2082	On	4233	846.6	2118.5
X04347_s_at	Human liver mRNA fragment DNA binding protein LPI homologous (C-terminal)	0	1324	830	On	911	182.2	455.5
M21142_cds2_s_at	guanine nucleotide-binding protein G-i-alpha-3 gene extracted from Human guanine nucleotide-binding protein alpha-subunit gene (G-i-alpha)	0	1100	839	On	782	188.4	301
J09106_s_at	Human beta-2 microglobulin gene "mRNA," 3' end	1137	9190	4802	Increased	3684	1642.4	2400.6
S82297_at	beta 2-microglobulin (11bp deleted between nucleotides 98-99) "Thuman," colon cancer cell line "HCT," mRNA "Mutant," 416 nt	610	4008	3900	Increased	2360	966.4	1489
M34616_at	Human omega light chain protein 14.1 (lg lambda chain related) gene	0	4080	6280	On	2235	447	1117.5
L02320_f_at	Human alpha (chain Hs lambda-17) lambda-like "gene," complete cds	0	373	734	On	0	0	0
M63438_s_at	Human Ig rearranged gamma chain "mRNA," V-J-C region and complete cds	0	1402	7075	On	4579	915.8	2289.5
M87700_s_at	Human (hybridoma H210) anti-hepatitis A IgG variable "region," constant "region," complementarity-determining regions "mRNA," complete cds	0	2420	4769	On	3447	689.4	1723.6
S71043_mna1_s_at	Ig alpha 2-murineoglobulin A heavy chain subtype 2 constant "region," germ line "Thuman," peripheral blood "nautrophils," "Genomic," 1789 nt	0	1175	2608	On	1473	284.8	736.6
M14481_mna1_s_at	PTMA gene extracted from Human prothymosin alpha "mRNA," complete cds	0	1410	948	On	841	128.2	320.6
M18052_at	Human pancreatic elastase 5A mRNA, complete cds	0	466	222	On	201	40.2	190.6
M81832_s_at	Human 3-adenosylhomocysteine hydrolase (AHCY) "mRNA," complete cds	0	233	128	On	71	14.2	36.6
M93484_at	Human act "gene," complete cds	0	294	213	On	159	31.8	78.6
X12871_mna1_at	Human act protein gene extracted from Human gene for heterogenous nuclear ribonucleoprotein (hnRNP) core protein A1	0	716	394	On	694	118.9	297
X16183_at	Human mRNA for 80-kDa heat-shock protein	880	1691	1790	Increased	919	652.6	782.6
Y08614_at	Human mRNA for CRU1 protein	0	171	136	On	72	14.4	36
Z49146_s_at	Human mRNA for ribosomal protein L20	616	2569	1601	Increased	2203	953.4	1459.5
Z48501_s_at	Human mRNA for polyadenylation binding protein II, fgb-Z48501 fntype=RNA	600	1893	2633	Increased	1263	760.6	911.6
HG3076-4T3230_s_at	Heterogeneous Nuclear Ribonucleoprotein "K," Alt. Splice 1	0	433	247	On	239	47.8	110.6
M36430_s_at	Human traneducin beta-1 subunit "mRNA," 3' end	0	808	265	On	118	23.6	69
HG417-4T417_s_at	Cathepsin B	0	2797	1783	On	1172	234.4	638
J02853_s_at	Human ADP/ATP carrier protein "mRNA," complete cds	0	301	408	On	337	67.4	168.6

Accession	Gene	0	425	348	On	0	3146.0	0	7088.5
U04046_s_at	Human calmodulin "mRNA," complete cds	0	425	348	On	0	3146.0	0	7088.5
M28311_s_at	Human cystic fibrosis antigen mRNA, complete cds	0	2359	1413	On	15733			
X13546_rna1_at	Human HMG-17 gene for non-fibrous chromosomal protein HMG-17.	208	740	1126	Increased	223	210.8	215	
X04220_at	Haaspiens deli mRNA	0	189	208	On	60	10	25	
X07325_at	Haaspiens p27 mRNA	0	360	683	On	0	0	0	
U0205_at	Human K6b (epidermal keratin, type II) gene	80	0	0	Off	154	94.8	117	
D10922_s_at	Human mRNA for PML-P-related receptor (H605)	405	0	0	Off	20	401.2	209.5	
D06843_s_at	Human spleen PAB1 (pseudouridine boundary-like sequence) "mRNA," clone Sp2. Apb-D06843 htypes-RNA	304	0	0	Off	0	201.2	182	
L11872_at	Human Kruppel related zinc finger protein (KTF10) "mRNA," complete cds	2099	1770	1219	Decreased	370	3028	2030	
U019370_at	Human spleen calbindin 27 gene, exons 1 and 2, and Alu repeat	385	0	0	Off	0	282	182.5	
Z15402_rna1_s_at	Haaspiens gene encoding "E-cadherin," exon 3 and joined CDS	782	230	242	Decreased	160	941.4	480.5	
M28695_at	Human histatin 2 (HIS2) mRNA, complete cds	210	0	0	Off	0	168	105	
D06233_s_at	Human glutathione transferase class mu number 4 (GSTM4) "gene," complete cds	12518	0	0	Off	0	10014.4	8260	
U03210_s_at	Human metabotropic glutamate receptor 1 alpha (mGluR1alpha) "mRNA," complete cds	317	0	0	Off	0	263.0	160.5	
U03830_at	Human NF-kappa-B p50delta3 "mRNA," spliced transcript lacking exons 8 and "7," partial cds. Hsp053838 htypes-RNA	478	0	0	Off	67	353.0	287.0	
U79295_at	Human clone 23901 mRNA sequence	164	0	0	Off	0	131.2	82	
U79304_at	Human clone 23908 "mRNA," partial cds.	99	0	0	Off	0	78.2	49.5	
X79260_at	Haaspiens mRNA for SYT-65X, synovial sarcoma translocation junction	844	0	0	Off	0	676.2	422	
X00703_s_at	Haaspiens gene for 5-HT2c receptor	689	0	0	Off	124	676	408.5	
X06846_at	Haaspiens mRNA for ribbed kinase kinase 2	2080	681	604	Decreased	0	1678.2	1049.5	
X06850-H1880_at	Human mucin 8, gastric (single repeat clone) -human (fragment), partial CDS	1793	0	493	Decreased	0	1434.4	896.5	
L08707_s_at	Human (clone L8) orphan G protein-coupled receptor "mRNA," complete cds	689	0	150	Decreased	109	493	340	
R27740_f_at	Human limonin/obolulin-related 14.1 protein "mRNA," complete cds	1118	0	0	Off	0	885.2	659.5	
R29335_at	Human 65HC class II DO-alpha mRNA, partial cds	1043	0	217	Decreased	0	894.4	621.5	
X06807_at	Haaspiens a-myb mRNA	289	0	0	Off	0	234.4	146.5	
X05632_s_at	Haaspiens mRNA for Arg protein tyrosine kinase-binding protein	281	0	0	Off	0	208.8	130.5	

Only genes scored as present are shown. *Deviation describes aberration from pool ** 20% and 50% describes expected units of expression if tumor pool was added 20% or 50% bladder wall components. Genes in bold do not need interrogation of bladder wall contribution. Off, genes that are turned off. On, genes that are turned on.

Table 5

Expression pattern				>=3 fold ch.	>=5 fold ch.	>=7 fold ch.	
N	↑	Ta	↑	T2-4	9 v	0	0
N	↑	Ta	→	T2-4	233 v	76	34
N	↑	Ta	↓	T2-4	164 v	51	23
N	→	Ta	↑	T2-4	612 v	262	141
N	→	Ta	→	T2-4	5407 v	6456	6768
N	→	Ta	↓	T2-4	264 v	92	41
N	↓	Ta	↑	T2-4	175 v	49	20
N	↓	Ta	→	T2-4	208 v	87	45
N	↓	Ta	↓	T2-4	2 v	0	0

Table 6

Connective tissue A													
Gene Name	Positiv	Negativ	Pairs	UPairs	IPos	Fractl	Log Avg	PM E	MM E	Pos/Neg	Avg Diff	Abs Call	
hum_alu_at	68	0	69	69	67	0.99	6.27	4	0	Inf	10744	P	
L08499_at	19	0	20	20	18	0.95	7.03	3	0	Inf	6084	P	
AFFX-HUMGAPDH/M33197_3_i	18	0	20	20	18	0.90	5.85	1	0	Inf	5588	P	
L10343_at	18	0	20	20	18	0.95	6.38	2	0	Inf	5388	P	
D23660_at	19	0	20	20	18	0.95	7.89	3	0	Inf	5345	P	
AFFX-HSAC07/X00351_M_at	20	0	20	20	18	1.00	6.41	0	0	Inf	5185	P	
D88422_at	18	0	20	20	18	0.90	7.09	5	0	Inf	5167	P	
HG3214-HT3391_at	19	0	20	20	18	0.95	6.77	3	0	Inf	4966	P	
M21005_at	10	3	20	20	18	0.50	1.87	0	0	3.3	4930	P	
HG2873-HT3017_at	19	0	20	20	18	0.95	7.24	4	0	Inf	4372	P	
HG3384-HT3541_at	19	0	20	20	18	0.95	7.09	4	0	Inf	4242	P	
HG3549-HT3751_at	20	0	20	20	18	1.00	6.49	2	0	Inf	3943	P	
M17885_at	20	0	20	20	18	1.00	6.88	2	0	Inf	3690	P	
AFFX-HSAC07/X00351_5_at	17	0	20	20	18	0.85	5.46	0	0	Inf	3657	P	
HG1800-HT1823_at	18	0	20	20	18	0.90	4.94	1	0	Inf	3582	P	
M17886_at	17	1	20	20	18	0.85	4.70	0	0	17.0	3488	P	
AFFX-HUMGAPDH/M33197_M_	18	0	20	20	18	0.90	5.29	0	0	Inf	3413	P	
M18000_at	20	0	20	20	18	1.00	7.08	4	0	Inf	3315	P	
M13834_cds2_at	17	0	20	20	18	0.85	5.00	1	0	Inf	3281	P	
AFFX-HSAC07/X00351_3_at	18	1	20	20	18	0.80	5.15	0	0	18.0	3211	P	
M11147_at	17	0	20	20	18	0.85	6.32	2	0	Inf	3172	P	
L08505_at	14	0	20	20	18	0.70	4.09	0	0	Inf	3024	P	
AFFX-CreX-3_at	20	0	20	20	17	1.00	6.01	1	0	Inf	3008	P	
M17793_at	18	1	20	20	18	0.90	6.09	1	0	18.0	2774	P	
D78361_at	17	1	20	20	18	0.85	4.91	0	0	17.0	2518	P	
L38941_at	20	0	20	20	18	1.00	6.50	1	0	Inf	2460	P	
D00017_at	18	0	20	20	18	0.90	4.24	0	0	Inf	2387	P	
AFFX-CreX-5_at	18	0	20	20	18	0.95	5.22	0	0	Inf	2382	P	
L14530_at	19	0	20	20	18	0.85	6.56	2	0	Inf	2193	P	
L11621-HT821_at	18	0	20	20	18	0.90	5.13	0	0	Inf	2159	P	
D38583_at	17	2	20	20	18	0.80	4.82	0	0	8.5	2101	P	
HG33-HT33_at	18	0	20	20	18	0.95	5.87	1	0	Inf	2077	P	
L19527_at	19	0	20	20	18	0.90	4.69	1	0	Inf	1981	P	
HG4319-HT4589_at	18	0	20	20	18	0.85	5.82	0	0	Inf	1960	P	
AFFX-HUMGAPDH/M33197_5_i	17	0	20	20	18	0.95	5.57	2	0	Inf	1939	P	
HG613-HT1613_at	13	1	20	20	17	0.90	5.59	1	0	Inf	1873	P	
L20941_at	15	2	20	20	18	0.75	3.44	2	0	13.0	1771	P	
M11353_at	15	2	20	20	18	0.85	5.61	4	0	7.5	1697	P	
D79205_at	20	0	20	20	18	1.00	6.59	1	0	Inf	1639	P	
AFFX-BioOn-3_at	12	2	20	20	17	0.60	2.53	0	0	6.0	1598	P	
M21388_at	15	0	20	20	18	0.75	3.40	0	0	Inf	1572	P	
D87735_at	17	0	20	20	18	0.85	4.85	1	0	Inf	1439	P	
J03827_at	14	1	20	20	18	0.70	3.89	2	0	14.0	1409	P	
HG384-HT384_at	12	0	20	20	18	0.60	4.02	3	0	Inf	1399	P	
L11566_at	15	0	20	20	18	0.75	3.76	0	0	Inf	1378	P	
HG4542-HT4947_at	12	1	20	20	18	0.60	4.06	0	0	12.0	1375	P	
L26247_at	18	1	20	20	18	0.90	5.33	2	0	18.0	1245	P	
D00854_at	19	0	20	20	18	0.95	4.77	0	0	Inf			

Slide 1

Connective tissue A																			
J00124_at	15	1	20	20	18 0.75	3.91	1	0	15.0	1210 P									
D45370_at	14	1	20	20	17 0.70	2.59	0	0	14.0	1127 P									
HG2279-HT2375_at	13	0	20	20	18 0.65	3.07	0	0	Inf	1112 P									
M19283_at	17	2	20	20	18 0.85	3.74	2	1	8.5	1086 P									
HG311-HT311_at	18	0	20	20	17 0.90	5.26	1	0	Inf	1067 P									
M13903_at	13	0	20	20	18 0.65	2.57	0	0	Inf	1000 P									
D14710_at	13	0	20	20	18 0.65	2.85	0	0	Inf	980 P									
HG2788-HT2896_at	16	0	20	20	18 0.80	3.13	0	0	Inf	973 P									
AC002115_cds1_at	11	0	20	20	18 0.55	2.71	0	0	Inf	941 P									
D86429_at	12	0	20	20	18 0.60	3.21	0	0	Inf	917 P									
J03592_at	16	0	20	20	18 0.80	3.50	0	0	Inf	905 P									
D50840_at	19	0	20	20	18 0.95	5.59	4	0	Inf	851 P									
D28068_at	18	1	20	20	18 0.80	3.30	0	1	16.0	821 P									
J03181_at	18	1	20	20	18 0.80	4.33	0	0	18.0	799 P									
HG1153-HT1163_at	9	0	20	20	18 0.45	2.17	0	0	Inf	772 P									
L24203_at	13	2	20	20	18 0.65	3.15	1	0	6.5	762 P									
D13746_at	11	0	20	20	17 0.55	2.04	0	0	Inf	744 P									
M19483_at	13	0	20	20	18 0.65	3.28	0	0	Inf	683 P									
D16217_at	12	0	20	20	18 0.50	2.35	0	0	Inf	681 P									
M15681_at	14	0	20	20	18 0.70	3.49	0	0	Inf	653 P									
HG987-HT987_at	13	2	20	20	18 0.35	1.71	1	0	6.5	640 P									
D21261_at	7	0	20	20	18 0.45	1.47	0	0	Inf	621 P									
AB001325_at	9	0	20	20	18 0.45	2.22	0	0	4.5	612 P									
L19886_ma1_at	9	2	20	20	18 0.55	2.52	0	0	Inf	611 P									
D13118_at	11	0	20	20	18 0.55	2.02	0	0	11.0	600 P									
D29012_at	11	1	20	20	18 0.50	2.05	0	0	Inf	588 P									
L09504_at	10	0	20	20	18 0.50	1.94	0	0	Inf	584 P									
M14200_ma1_at	14	0	20	20	18 0.70	3.59	2	0	Inf	581 P									
L08686_at	12	1	20	20	18 0.60	2.66	0	0	12.0	567 P									
D31883_at	15	1	20	20	18 0.75	3.68	0	0	15.0	561 P									
D16562_at	12	0	20	20	18 0.60	3.01	0	0	Inf	559 P									
D88667_at	12	0	20	20	18 0.65	2.14	0	0	13.0	558 P									
J04823_ma1_at	13	1	20	20	18 0.55	2.36	0	0	5.5	557 P									
D85815_at	11	2	20	20	18 0.60	2.29	0	0	12.0	554 P									
D11428_at	12	1	20	20	18 0.60	1.97	0	0	Inf	552 P									
D26308_at	12	1	20	20	18 0.50	1.83	0	0	Inf	549 P									
D26124_at	10	0	20	20	18 0.70	2.87	0	0	14.0	546 P									
J01456_at	14	1	20	20	18 0.75	2.67	0	0	Inf	539 P									
J04173_at	15	0	20	20	18 0.80	3.30	0	0	Inf	532 P									
D87953_at	16	0	20	20	18 0.45	1.87	0	0	Inf	527 P									
L19437_at	9	0	20	20	18 0.55	2.79	0	0	Inf	505 P									
J04988_at	11	0	20	20	18 0.45	1.79	0	0	Inf	500 P									
L38486_at	9	0	20	20	18 0.45	1.46	0	0	Inf	499 P									
D87292_at	9	0	20	20	18 0.70	3.27	0	0	Inf	485 P									
J02874_at	14	0	20	20	18 0.50	2.07	1	0	10.0	484 P									
M19961_at	10	1	20	20	18 0.70	2.36	0	0	Inf	481 P									
D00632_at	14	0	20	20	18 0.65	2.50	0	0	Inf	475 P									
D38047_at	13	0	20	20	18 0.55	2.27	0	0	4.3	457 P									
HG662-HT662_at	13	3	20	20	18 0.55	2.27	0	0	0.90										
D14520_at	9	1	20	20	18 0.45	1.54	0	0											

Side 2

Connective tissue A

K02765_at	13	1	20	20	18 0.85	1.66	0	0	0 13.0	455 P
AFFX-BioDn-5_at	11	1	20	20	18 0.55	1.60	0	0	0 11.0	450 P
HG174-HIT174_at	11	0	20	20	18 0.55	2.00	0	0	0 Inf	433 P
M16279_at	10	0	20	20	17 0.50	1.73	0	0	0 Inf	418 P
D23662_at	9	0	20	20	18 0.45	1.53	0	0	0 Inf	417 P
J02854_at	10	1	20	20	17 0.50	2.07	0	0	0 10.0	412 P
M16728_at	13	3	20	20	18 0.65	2.45	1	0	0 4.3	412 P
HG3494-HIT3688_at	13	1	20	20	17 0.40	1.35	0	0	0 8.0	410 P
J04080_at	13	1	20	20	18 0.65	3.09	0	0	0 13.0	407 P
D98548_at	7	0	20	20	18 0.35	1.52	0	0	0 Inf	404 P
D88479_at	8	0	20	20	18 0.40	1.57	0	0	0 Inf	404 P
D31846_at	8	1	20	20	18 0.40	1.35	0	0	0 8.0	402 P
D83874_at	8	0	20	20	18 0.45	2.26	0	0	0 Inf	398 P
D14812_at	8	0	20	20	18 0.45	1.51	0	0	0 Inf	396 P
J03040_at	8	0	20	20	18 0.40	2.06	0	0	0 Inf	393 P
AFFX-HSAC07X00361_3_at	12	0	20	20	17 0.60	2.80	0	0	0 Inf	392 P
L27843_at	8	0	20	20	17 0.40	1.47	0	0	0 4.3	391 P
D30655_at	13	3	20	20	18 0.65	3.06	0	0	0 4.3	391 P
J02902_at	7	1	20	20	18 0.35	1.95	0	0	0 7.0	391 P
L12168_at	10	0	20	20	18 0.50	2.54	0	0	0 Inf	390 P
L10284_at	14	0	20	20	18 0.70	3.39	0	0	0 Inf	388 P
D26598_at	10	1	20	20	18 0.50	1.87	0	0	0 10.0	387 P
L76200_at	11	1	20	20	18 0.55	1.89	0	0	0 11.0	384 P
J03459_at	8	3	20	20	18 0.45	1.81	1	0	0 3.0	381 P
D90209_at	14	0	20	20	17 0.70	3.34	0	0	0 Inf	380 P
D25274_at	14	2	20	20	17 0.70	2.26	0	0	0 7.0	378 P
D26598_at	10	0	20	20	18 0.50	1.86	0	0	0 Inf	359 P
L19605_at	10	0	20	20	17 0.50	1.66	0	0	0 Inf	336 P
AFFX-BioC-5_at	10	1	20	20	18 0.50	1.64	0	0	0 10.0	333 P
D78151_at	10	0	20	20	18 0.50	1.81	0	0	0 Inf	319 P
AJ000480_at	8	1	20	20	18 0.40	1.70	0	0	0 8.0	314 P
D23673_at	11	2	20	20	17 0.55	1.79	0	0	0 5.5	312 P
L11370_at	10	0	20	20	18 0.50	1.98	0	0	0 Inf	311 P
D00761_at	10	0	20	20	18 0.50	1.77	0	0	0 Inf	310 P
L49169_at	10	0	20	20	18 0.50	1.99	1	0	0 Inf	306 P
D83779_at	8	1	20	20	17 0.45	1.49	1	0	0 9.0	304 P
D28416_at	13	2	20	20	18 0.35	2.07	1	0	0 7.0	301 P
D25218_at	7	1	20	20	18 0.35	2.88	2	0	0 6.5	300 P
D45248_at	13	2	20	20	18 0.65	2.88	0	0	0 Inf	300 P
J04611_at	8	0	20	20	18 0.40	1.62	0	0	0 7.0	295 P
D63475_at	12	1	20	20	18 0.35	1.48	0	0	0 7.0	290 P
L13381_at	7	1	20	20	18 0.60	1.95	0	0	0 Inf	289 P
L25080_at	12	0	20	20	18 0.60	3.00	0	0	0 Inf	288 P
HG1862-HIT1897_at	11	0	20	20	18 0.55	1.47	0	0	0 Inf	284 P
AJ001421_at	7	0	20	20	18 0.35	1.72	0	0	0 5.0	281 P
K03195_at	14	1	20	20	18 0.70	3.33	3	0	0 14.0	274 P
L07633_at	12	1	20	20	17 0.60	2.38	0	0	0 12.0	270 P
D38048_at	10	0	20	20	18 0.50	2.40	0	0	0 Inf	264 P
L08246_at	10	2	20	20	18 0.50	1.76	1	0	0 5.0	260 P
AF005775_at	8	0	20	20	18 0.45	1.84	0	0	0 Inf	253 P

Side 3

Connective tissue A

D50310_at	9	1	20	20	18.045	1.79	0	0.90	247 P
HG1112-HT112_at	11	1	20	20	18.055	1.83	0	0.110	244 P
L11285_at	9	2	20	20	18.045	1.67	0	0.45	244 P
D14689_at	8	2	20	20	18.040	1.35	0	0.40	242 P
D65654_at	10	1	20	20	18.050	2.28	0	0.100	242 P
D28423_at	9	1	20	20	17.045	2.26	0	0.80	241 P
D31765_at	8	1	20	20	18.040	2.07	1	0.80	240 P
HG2855-HT295_at	8	2	20	20	18.040	1.95	0	0.40	240 P
M14058_at	10	1	20	20	18.050	2.37	0	0.100	240 P
D49400_at	9	2	20	20	17.045	1.66	1	1.45	239 P
D87258_at	8	1	20	20	18.040	1.48	0	0.80	238 P
D26128_at	7	0	20	20	17.035	1.17	0	0.1nf	237 P
L32977_at	13	1	20	20	18.065	2.73	0	0.130	237 P
D31767_at	8	2	20	20	17.040	1.33	0	0.40	236 P
D61380_at	10	2	20	20	18.050	1.67	0	0.50	231 P
D13988_at	10	0	20	20	18.035	1.33	0	0.1nf	228 P
AFFX-BioC-3_at	7	0	20	20	18.035	1.42	0	0.1nf	225 P
L76191_at	8	1	20	20	18.040	2.28	1	0.80	223 P
D42123_at	9	1	20	20	18.045	1.20	0	0.90	223 P
D11094_at	8	2	20	20	18.040	1.19	0	0.40	222 P
L25085_at	7	0	20	20	18.035	1.77	0	0.1nf	222 P
D29643_at	12	2	20	20	18.060	1.88	0	0.60	221 P
L11373_at	8	2	20	20	18.040	1.34	0	0.40	214 P
D17525_at	7	1	20	20	18.035	1.43	0	0.70	211 P
D21260_at	7	0	20	20	18.035	1.14	0	0.1nf	211 P
D28364_at	13	0	20	20	18.065	2.59	1	0.1nf	209 P
D63878_at	9	2	20	20	18.045	1.28	0	1.45	206 P
D78134_at	7	1	20	20	18.035	1.18	0	0.70	203 P
D38549_at	7	1	20	20	18.035	1.68	2	1.70	201 P
M14010_at	9	1	20	20	18.045	1.96	0	0.90	201 P
D21853_at	9	1	20	20	18.045	1.84	0	0.90	199 P
L40401_at	8	0	20	20	18.040	1.82	0	0.1nf	197 P
D63476_at	8	2	20	20	18.045	1.42	0	0.45	195 P
L40027_at	8	0	20	20	18.040	1.93	1	0.1nf	193 P
D00762_at	10	0	20	20	18.050	2.12	0	0.1nf	188 P
D17400_at	9	2	20	20	18.045	1.50	0	0.45	187 P
L03532_at	11	3	20	20	18.055	1.71	0	0.37	187 P
L08486_at	12	1	20	20	17.060	3.01	1	0.120	187 P
HG3995-HT4255_at	8	1	20	20	18.040	1.14	0	0.80	186 P
M11717_ma1_at	13	2	20	20	18.065	3.65	2	0.65	186 P
D13370_at	9	1	20	20	17.045	1.75	0	0.90	185 P
HG1116-HT1116_at	8	0	20	20	18.040	1.46	0	0.1nf	184 P
K03515_at	8	2	20	20	18.040	1.32	0	0.40	183 P
D17516_at	7	0	20	20	17.035	1.45	0	0.1nf	177 P
HG4272-HT4542_at	7	1	20	20	18.035	1.97	1	0.70	177 P
D28137_at	9	3	20	20	18.045	1.55	0	0.30	176 P
L22009_at	8	2	20	20	18.040	1.35	0	0.40	175 P
D44466_at	12	1	20	20	18.060	2.09	1	0.120	173 P
L29277_at	8	0	20	20	17.040	1.41	0	0.1nf	173 P
L00352_at	7	1	20	20	18.035	1.98	1	0.70	169 P

Side 4

Connective tissue A

L34587_at	7	1	20	20	18.035	1.46	0	0.7.0	168 P
L37042_at	9	0	20	20	18.045	1.42	0	0 Inf	168 P
D86966_at	8	2	20	20	18.040	1.35	0	0.4.0	168 P
D16050_at	11	0	20	20	17.055	1.77	0	0 Inf	166 P
L10838_at	8	0	20	20	18.040	1.16	0	0 Inf	166 P
D14043_at	10	1	20	20	18.050	1.73	0	0 10.0	159 P
D87071_at	8	2	20	20	17.040	1.12	0	0.4.0	157 P
D42043_at	11	2	20	20	18.035	2.07	0	0.5.5	155 P
L38932_at	9	0	20	20	18.045	1.29	0	0 Inf	152 P
D90276_at	9	1	20	20	18.045	1.85	1	0.8.0	148 P
M13450_at	13	3	20	20	18.065	2.36	0	0.4.3	148 P
M11726_at	9	2	20	20	18.045	1.35	0	0.4.5	147 P
L41690_at	9	2	20	20	18.045	1.90	0	0.4.5	146 P
D43950_at	7	0	20	20	18.035	1.52	0	0 Inf	145 P
D63851_at	8	2	20	20	18.040	1.12	0	0.4.0	143 P
L19314_at	7	0	20	20	17.035	1.64	0	0 Inf	143 P
L41668_ma1_at	8	0	20	20	17.040	1.87	0	0 Inf	142 P
D83004_at	9	1	20	20	17.045	1.89	0	1.9.0	141 P
K02574_at	9	1	20	20	18.045	1.80	1	0.9.0	138 P
M13782_at	10	2	20	20	18.050	2.18	0	0.5.0	138 P
HG2415-HT2511_at	10	2	20	20	18.050	1.29	0	0.5.0	135 P
L20773_at	8	2	20	20	18.040	1.39	0	1.4.0	134 P
D10923_at	8	1	20	20	18.040	1.66	0	0.8.0	132 P
M12759_at	10	2	20	20	18.050	1.70	1	0.5.0	131 P
M16038_at	7	0	20	20	18.035	1.77	0	0 Inf	131 P
D86963_at	8	1	20	20	19.040	1.52	0	0.8.0	128 P
J05248_at	10	0	20	20	17.050	2.26	0	0 Inf	128 P
D90084_at	7	1	20	20	18.035	1.11	0	0.7.0	124 P
AF007875_at	8	1	20	20	18.040	1.33	0	0.8.0	123 P
D00726_at	7	0	20	20	18.035	1.62	0	0 Inf	123 P
J05243_at	9	0	20	20	18.045	1.62	0	0 Inf	122 P
L13761_ma1_at	7	0	20	20	18.035	1.52	0	0 Inf	119 P
L36951_at	10	0	20	20	18.050	1.86	0	0 Inf	119 P
M18533_at	12	2	20	20	18.060	3.76	4	0.6.0	119 P
J04605_at	7	1	20	20	18.035	1.22	0	0.7.0	117 P
D38553_at	7	2	20	20	18.035	1.48	0	0 Inf	116 P
L36531_at	7	0	20	20	18.035	1.46	1	0.3.5	116 P
L14837_at	9	2	20	20	18.045	2.20	2	0.4.5	113 P
HG4102-HT4372_at	7	1	20	20	18.035	1.12	0	0.7.0	109 P
L40395_at	8	2	20	20	18.040	1.38	0	0.4.0	107 P
D30756_at	8	1	20	20	17.040	2.08	2	0.8.0	106 P
L47738_at	8	0	20	20	18.040	0.90	0	0 Inf	105 P
D13641_at	9	3	20	20	18.045	1.05	0	0.8.0	104 P
D45399_at	9	3	20	20	18.045	1.65	0	0.3.0	104 P
L27706_at	12	2	20	20	18.060	1.93	0	0.6.0	104 P
D50683_at	8	3	20	20	18.045	1.47	0	0.3.0	100 P
HG2167-HT2237_at	9	1	20	20	18.045	1.19	0	0.9.0	99 P
D29641_at	7	1	20	20	18.035	1.43	0	0.7.0	98 P
L13977_at	7	1	20	20	18.035	1.58	1	0.7.0	97 P
L34600_at	7	0	20	20	18.035	1.05	0	0 Inf	95 P

Side 5

	Connective tissue A										
D42053_at	8	1	20	20	18 0.40	1.47	0	0.8 0	94 P		
M14123_xp12_at	9	3	20	20	18 0.45	1.36	1	0.3 0	93 P		
D14658_at	7	1	20	20	18 0.35	0.92	0	0.7 0	92 P		
L27841_at	8	2	20	20	18 0.40	1.00	0	0.4 0	91 P		
AF010193_at	7	1	20	20	18 0.35	1.07	0	0.7 0	90 P		
D50926_at	11	2	20	20	18 0.55	1.24	0	0.5 5	89 P		
M11321_at	10	1	20	20	18 0.50	1.35	0	0.10 0	88 P		
HG1102-HT1102_at	7	1	20	20	18 0.35	1.68	1	0.7 0	87 P		
L40393_at	12	2	20	20	17 0.60	2.43	0	0.6 0	86 P		
D80003_at	9	1	20	20	18 0.45	1.59	1	0.9 0	85 P		
M14219_at	10	1	20	20	18 0.50	1.99	1	0.10 0	84 P		
M14536_at	7	0	20	20	18 0.35	0.98	0	0. Inf	83 P		
M13695_at	9	3	20	20	18 0.45	2.24	1	0.3 0	82 P		
L19711_at	8	0	20	20	18 0.40	1.67	0	0. Inf	81 P		
L76703_at	9	2	20	20	18 0.45	2.08	1	0.4 5	80 P		
O63390_at	10	1	20	20	18 0.50	2.52	2	0.10 0	79 P		
HG831-HT831_at	9	2	20	20	18 0.45	1.31	1	0.4 5	78 P		
D21255_at	9	1	20	20	18 0.45	1.63	1	0.9 0	77 P		
D76129_at	9	3	20	20	18 0.45	1.60	1	0.3 0	76 P		
L48513_at	13	3	20	20	18 0.65	1.87	1	1.4 3	75 P		
M14636_at	9	3	20	20	18 0.45	1.62	1	2.3 0	74 P		
M15795_at	7	2	20	20	18 0.35	1.66	0	0.3 5	73 P		
HG1103-HT1103_at	9	2	20	20	18 0.45	1.51	1	0.4 5	71 P		
L35240_at	7	1	20	20	18 0.35	1.02	0	0.7 0	67 P		
L77886_at	9	3	20	20	17 0.45	2.27	2	0.3 0	59 P		
D14659_at	9	3	20	20	18 0.45	1.81	1	0.3 0	54 P		
J04156_at	8	2	20	20	18 0.40	1.23	1	0.4 0	54 P		
D87457_at	7	2	20	20	18 0.40	2.72	4	0.4 0	48 P		
L20321_at	8	1	20	20	18 0.35	0.92	1	0.7 0	32 P		
L20814_at	9	3	20	20	18 0.45	1.61	1	1.3 0	28 P		

Connective tissue B													
Gene Nam	Positive	Negative	Pairs	Pairs Usd	InAv	Pos	Fractl	Log Avg	PM Exces	MM Exces	Pos/Neg	Avg Diff	Abs Call
hum_alu_a	69	0	69	69	67	1.00	7.19	7.19	12	0	Inf	12502 P	
U46692_m	19	0	20	20	18	0.95	7.15	7.15	3	0	Inf	10030 P	
AFFX-HUN	18	0	20	20	18	0.90	6.05	6.05	0	0	Inf	5799 P	
AFFX-HSA	20	0	20	20	18	1.00	6.50	6.50	0	0	Inf	5422 P	
U14969_at	20	0	20	20	18	1.00	6.79	6.79	0	0	Inf	4539 P	
M60854_at	19	1	20	20	18	0.95	6.50	6.50	2	0	19.0	4473 P	
AFFX-Cre	18	0	20	20	18	0.95	7.67	7.67	3	0	Inf	4430 P	
M81757_at	18	0	20	20	18	0.90	6.62	6.62	2	0	Inf	4389 P	
U14973_at	19	0	20	20	18	0.95	6.06	6.06	1	0	Inf	4281 P	
AFFX-HSA	19	0	20	20	18	0.95	6.11	6.11	1	0	Inf	4114 P	
U14970_at	18	0	20	20	18	0.95	6.15	6.15	2	0	Inf	3928 P	
U14968_at	18	0	20	20	18	0.90	7.18	7.18	3	0	Inf	3885 P	
U14972_at	17	0	20	20	18	0.85	5.60	5.60	2	0	Inf	3695 P	
M84711_at	17	1	20	20	18	0.85	7.59	7.59	5	1	17.0	3651 P	
AFFX-HUN	17	0	20	20	18	0.85	5.08	5.08	0	0	Inf	3483 P	
M24194_at	19	0	20	20	18	0.95	5.89	5.89	0	0	Inf	3378 P	
U12465_at	19	0	20	20	18	0.95	6.01	6.01	0	0	Inf	3327 P	
M64716_at	17	2	20	20	18	0.85	5.15	5.15	3	0	8.5	3228 P	
S79522_at	19	0	20	20	18	0.95	6.42	6.42	4	0	Inf	3161 P	
AFFX-Cre	19	0	20	20	18	0.95	6.86	6.86	1	0	Inf	2966 P	
AFFX-HSA	18	0	20	20	17	0.90	5.87	5.87	0	0	Inf	2793 P	
AFFX-HUN	17	0	20	20	18	0.85	5.95	5.95	4	0	Inf	2690 P	
U14971_at	18	0	20	20	18	0.90	5.27	5.27	1	0	Inf	2645 P	
M77232_at	20	0	20	20	18	1.00	7.99	7.99	6	0	Inf	2616 P	
M94856_at	18	0	20	20	18	0.90	8.28	8.28	10	0	Inf	2522 P	
U12404_at	20	0	20	20	18	1.00	6.77	6.77	2	0	Inf	2506 P	
U09953_at	18	1	20	20	18	0.90	6.29	6.29	3	0	18.0	2488 P	
M32053_at	20	0	20	20	18	1.00	6.29	6.29	0	0	Inf	2129 P	
U58682_at	15	1	20	20	18	0.75	4.14	4.14	1	0	15.0	2053 P	
U49869_m	18	0	20	20	17	0.90	5.83	5.83	2	0	Inf	2005 P	
M32405_at	13	2	20	20	17	0.65	3.40	3.40	1	0	6.5	1876 P	
M31520_at	20	0	20	20	18	1.00	6.23	6.23	4	0	Inf	1875 P	
M84526_at	14	1	20	20	18	0.70	3.38	3.38	3	0	Inf	1819 P	
M38591_at	19	0	20	20	18	0.95	6.10	6.10	1	0	Inf	1735 P	
M95787_at	17	0	20	20	18	0.85	4.53	4.53	0	0	Inf	1655 P	
M97815_at	17	0	20	20	18	0.85	4.05	4.05	0	0	Inf	1653 P	
M86400_at	18	0	20	20	18	0.90	5.75	5.75	3	0	Inf	1565 P	
AFFX-BicC	15	2	20	20	17	0.80	3.26	3.26	0	0	Inf	1506 P	
M26860_at	16	0	20	20	18	0.80	7.17	7.17	9	0	Inf	1489 P	
M63138_at	12	1	20	20	18	0.60	2.92	2.92	0	0	12.0	1449 P	
M57710_at	18	1	20	20	18	0.90	6.45	6.45	2	1	18.0	1448 P	
M23613_at	17	1	20	20	18	0.85	5.57	5.57	4	0	17.0	1423 P	
M33680_at	15	0	20	20	18	0.75	3.69	3.69	1	0	Inf	1363 P	
M27891_at	14	0	20	20	18	0.70	3.55	3.55	0	0	Inf	1310 P	
S81914_at	18	0	20	20	18	0.90	5.75	5.75	1	0	Inf	1265 P	
U25789_at	16	0	20	20	18	0.80	5.97	5.97	2	0	Inf	1233 P	
M74542_at	14	1	20	20	18	0.75	3.88	3.88	0	0	14.0	1172 P	
M36690_at	15	1	20	20	18	0.75	3.97	3.97	0	0	15.0	1151 P	
S66738_at	16	1	20	20	18	0.80	5.75	5.75	0	0	15.0	924 P	
M34182_at	7	2	20	20	18	0.35	1.43	1.43	0	0	3.5		

Side 1

Connective tissue B																			
02934_al	18	1	20	20	18.00	4.82	0	0	0	0	0	0	0	0	0	0	0	0	0
33379_al	16	0	20	20	18.00	3.59	0	0	0	0	0	0	0	0	0	0	0	0	0
M50047_al	17	0	20	20	18.05	4.42	1	1	1	1	1	1	1	1	1	1	1	1	1
U17077_al	15	0	20	20	18.05	3.94	0	0	0	0	0	0	0	0	0	0	0	0	0
M76378_al	13	0	20	20	18.05	4.01	0	0	0	0	0	0	0	0	0	0	0	0	0
M93056_al	14	0	20	20	18.07	4.58	1	1	1	1	1	1	1	1	1	1	1	1	1
U15008_al	15	0	20	20	17.07	3.48	0	0	0	0	0	0	0	0	0	0	0	0	0
M64332_al	12	1	20	20	18.00	2.32	0	0	0	0	0	0	0	0	0	0	0	0	0
M69043_al	14	1	20	20	18.07	4.12	2	2	2	2	2	2	2	2	2	2	2	2	2
U32944_al	15	1	20	20	17.07	4.21	0	0	0	0	0	0	0	0	0	0	0	0	0
M55593_al	12	1	20	20	18.00	2.46	0	0	0	0	0	0	0	0	0	0	0	0	0
U09813_al	15	0	20	20	18.05	4.39	0	0	0	0	0	0	0	0	0	0	0	0	0
M98447_al	10	0	20	20	18.00	2.31	0	0	0	0	0	0	0	0	0	0	0	0	0
U41635_al	13	0	20	20	18.05	1.97	0	0	0	0	0	0	0	0	0	0	0	0	0
U51478_al	15	1	20	20	18.07	4.38	0	0	0	0	0	0	0	0	0	0	0	0	0
M66849_al	13	1	20	20	18.05	4.24	1	1	1	1	1	1	1	1	1	1	1	1	1
U04313_al	14	0	20	20	18.07	3.59	0	0	0	0	0	0	0	0	0	0	0	0	0
U48959_al	14	1	20	20	18.07	3.07	1	1	1	1	1	1	1	1	1	1	1	1	1
U46751_al	13	1	20	20	18.05	3.61	0	0	0	0	0	0	0	0	0	0	0	0	0
S77366_al	12	2	20	20	18.00	3.32	1	1	1	1	1	1	1	1	1	1	1	1	1
M23254_al	15	1	20	20	18.05	1.35	0	0	0	0	0	0	0	0	0	0	0	0	0
U44839_al	9	2	20	20	18.05	3.06	0	0	0	0	0	0	0	0	0	0	0	0	0
M62982_al	13	2	20	20	18.00	0.98	0	0	0	0	0	0	0	0	0	0	0	0	0
M88468_al	8	2	20	20	18.05	3.45	2	2	2	2	2	2	2	2	2	2	2	2	2
U21128_al	11	3	20	20	18.05	2.95	0	0	0	0	0	0	0	0	0	0	0	0	0
U60523_al	12	2	20	20	18.00	2.64	0	0	0	0	0	0	0	0	0	0	0	0	0
U30255_al	11	0	20	20	17.05	2.50	0	0	0	0	0	0	0	0	0	0	0	0	0
M60858_al	16	0	20	20	18.00	3.50	1	1	1	1	1	1	1	1	1	1	1	1	1
U37690_al	10	0	20	20	18.05	2.08	0	0	0	0	0	0	0	0	0	0	0	0	0
S45630_al	11	0	20	20	18.05	1.96	0	0	0	0	0	0	0	0	0	0	0	0	0
M98539_al	13	2	20	20	18.05	2.84	0	0	0	0	0	0	0	0	0	0	0	0	0
S75463_al	10	1	20	20	18.00	1.71	0	0	0	0	0	0	0	0	0	0	0	0	0
M28540_al	15	2	20	20	18.05	3.66	0	0	0	0	0	0	0	0	0	0	0	0	0
M80563_al	13	0	20	20	18.05	2.43	0	0	0	0	0	0	0	0	0	0	0	0	0
M22538_al	13	0	20	20	18.05	2.32	0	0	0	0	0	0	0	0	0	0	0	0	0
M75126_al	11	0	20	20	18.05	2.14	0	0	0	0	0	0	0	0	0	0	0	0	0
U56637_al	12	0	20	20	18.00	2.95	0	0	0	0	0	0	0	0	0	0	0	0	0
U46499_al	14	1	20	20	17.07	3.14	0	0	0	0	0	0	0	0	0	0	0	0	0
U12779_al	7	0	20	20	18.05	1.00	0	0	0	0	0	0	0	0	0	0	0	0	0
U51004_al	13	1	20	20	18.05	2.57	0	0	0	0	0	0	0	0	0	0	0	0	0
U11881_al	8	1	20	20	18.00	1.49	0	0	0	0	0	0	0	0	0	0	0	0	0
U03057_al	12	0	20	20	17.00	2.03	0	0	0	0	0	0	0	0	0	0	0	0	0
M96739_al	12	0	20	20	18.05	1.37	0	0	0	0	0	0	0	0	0	0	0	0	0
M22760_al	13	0	20	20	18.05	3.54	0	0	0	0	0	0	0	0	0	0	0	0	0
U62962_al	8	0	20	20	18.00	1.65	0	0	0	0	0	0	0	0	0	0	0	0	0
AFFX-BioC	12	2	20	20	18.00	1.72	0	0	0	0	0	0	0	0	0	0	0	0	0
S73591_al	13	2	20	20	18.05	2.35	0	0	0	0	0	0	0	0	0	0	0	0	0
M63391_al	8	1	20	20	18.00	1.61	0	0	0	0	0	0	0	0	0	0	0	0	0
M88338_al	11	2	20	20	18.05	1.48	0	0	0	0	0	0	0	0	0	0	0	0	0
M76482_al	14	3	20	20	18.07	2.79	0	0	0	0	0	0	0	0	0	0	0	0	0
M22382_al	13	0	20	20	18.05	2.58	0	0	0	0	0	0	0	0	0	0	0	0	0
M22490_al	8	1	20	20	18.00	1.47	0	0	0	0	0	0	0	0	0	0	0	0	0

Side 2

Connective tissue B

M57567_al	9	1	20	20	18.045	1.77	0	0.9.0	377 P
U15932_at	14	1	20	20	18.070	3.10	0	1.14.0	375 P
AFFX-HSA	12	0	20	20	17.060	2.29	0	0 Inf	374 P
S74017_at	15	2	20	20	18.075	2.72	0	0.7.5	372 P
M74491_al	12	0	20	20	18.060	2.09	0	0 Inf	363 P
U37519_al	11	1	20	20	18.055	2.22	0	0.11.0	358 P
U29084_al	15	1	20	20	18.075	3.51	1	1.15.0	353 P
U62402_al	9	0	20	20	18.045	1.99	0	0 Inf	350 P
U29953_m	12	0	20	20	18.060	2.57	0	0 Inf	349 P
U46025_at	11	0	20	20	18.055	1.97	0	0 Inf	349 P
U46570_al	9	1	20	20	18.045	1.53	0	0.9.0	347 P
S73149_at	8	0	20	20	18.040	1.20	0	0 Inf	346 P
U33821_al	10	1	20	20	18.050	1.94	0	0.10.0	344 P
U09117_al	8	2	20	20	18.040	1.33	0	0.4.0	340 P
AFFX-BioC	15	2	20	20	18.075	2.38	0	0.7.5	340 P
M37104_at	17	0	20	20	18.085	3.43	2	0 Inf	338 P
M59815_at	10	2	20	20	17.050	2.14	0	0.5.0	337 P
M75099_al	9	1	20	20	18.045	1.69	0	0.9.0	331 P
U07857_at	17	1	20	20	17.055	3.44	0	0.17.0	330 P
M28209_al	13	0	20	20	18.065	2.74	0	0 Inf	321 P
U02020_at	15	2	20	20	18.075	3.40	0	0.7.5	315 P
M31525_al	10	3	20	20	18.050	1.92	0	0.3.3	314 P
M60278_at	9	2	20	20	18.045	2.06	0	0.4.5	308 P
M83751_at	13	0	20	20	18.065	2.21	0	0 Inf	307 P
M63167_at	10	1	20	20	17.050	1.51	0	0.10.0	306 P
U15085_at	13	0	20	20	18.085	2.34	0	0 Inf	306 P
M55621_at	12	0	20	20	17.060	2.65	0	0 Inf	304 P
S72487_at	8	0	20	20	18.040	1.71	0	0 Inf	301 P
U00968_at	10	0	20	20	18.050	1.12	0	0 Inf	301 P
M94630_at	9	2	20	20	18.045	1.31	1	0.4.5	290 P
M59465_at	11	2	20	20	18.055	2.88	2	0.5.5	289 P
M37583_at	13	1	20	20	18.065	3.67	1	0.13.0	288 P
M84349_al	11	1	20	20	17.055	2.58	0	0.11.0	286 P
M99701_at	13	1	20	20	18.065	2.72	1	0.13.0	282 P
U37122_at	10	1	20	20	17.050	1.95	1	0.10.0	282 P
U57342_at	7	0	20	20	18.035	1.06	0	0 Inf	281 P
M34079_al	9	3	20	20	17.045	1.53	0	0.3.0	280 P
S68616_at	8	2	20	20	18.040	1.35	0	0.4.0	279 P
M69066_al	14	2	20	20	17.070	3.20	0	0.7.0	278 P
M88279_al	11	0	20	20	18.055	2.06	0	0 Inf	276 P
M31013_al	12	2	20	20	18.060	2.13	0	0.6.0	274 P
M84345_al	11	1	20	20	18.055	1.77	0	0.11.0	274 P
U37689_at	8	0	20	20	18.040	1.35	0	0 Inf	269 P
U41515_at	11	1	20	20	18.055	2.31	0	0.11.0	269 P
M37984_at	8	2	20	20	18.060	1.43	0	0.4.0	267 P
M88458_at	12	0	20	20	18.055	1.93	0	0 Inf	265 P
U02570_at	11	1	20	20	18.045	2.28	1	0.11.0	263 P
M68864_at	9	1	20	20	18.045	2.10	0	0.8.0	260 P
M31984_at	11	1	20	20	18.055	2.60	0	0.11.0	257 P
M35678_at	10	2	20	20	18.050	1.55	0	1.5.0	255 P
U62015_at	8	0	20	20	18.040	1.58	0	0 Inf	253 P
U44755_al	7	1	20	20	18.035	1.45	0	0.7.0	250 P

Side 3

Connective tissue B									
M80244_al	9	1	20	20	17.045	1.50	0	0.9.0	249 P
U02493_al	9	1	20	20	18.045	2.04	0	0.8.0	247 P
M29696_al	8	1	20	20	18.040	1.21	0	0.8.0	246 P
M73720_al	12	0	20	20	17.060	2.59	0	0.1nf	245 P
U09579_at	9	2	20	20	18.045	2.07	1	0.4.5	242 P
M92303_al	7	2	20	20	18.035	1.41	0	0.3.5	240 P
U20285_al	7	1	20	20	18.035	1.80	0	0.7.0	240 P
U50733_al	9	1	20	20	18.045	1.83	0	0.9.0	239 P
M29536_al	13	2	20	20	18.065	2.11	0	0.6.5	238 P
M63483_al	11	3	20	20	18.055	1.75	0	0.3.7	238 P
M83186_al	10	3	20	20	18.050	1.87	0	0.3.3	238 P
U40391_m	9	1	20	20	18.045	1.50	0	0.9.0	237 P
M86667_al	13	0	20	20	18.065	3.08	1	0.1nf	233 P
SS3911_al	11	2	20	20	17.055	1.84	0	0.5.5	233 P
AFEX-BioC	10	1	20	20	18.050	1.81	0	0.10.0	232 P
M33308_al	13	0	20	20	18.065	3.20	1	0.1nf	231 P
S83364_al	9	1	20	20	18.045	2.20	0	0.9.0	231 P
U06863_at	7	0	20	20	18.035	1.14	0	0.1nf	230 P
M37033_al	11	3	20	20	18.055	1.97	1	0.3.7	229 P
U21931_at	9	2	20	20	18.045	1.55	0	0.4.5	229 P
M36341_al	13	1	20	20	17.065	2.63	0	0.13.0	225 P
M55040_al	8	2	20	20	18.040	1.18	0	0.4.0	225 P
M80254_al	8	1	20	20	18.040	1.69	0	0.8.0	223 P
M57763_al	7	2	20	20	18.035	1.35	0	0.3.5	222 P
M83088_al	8	2	20	20	18.040	1.71	0	0.4.0	221 P
M33336_al	16	1	20	20	18.080	2.70	0	0.16.0	217 P
M58028_at	9	1	20	20	18.045	1.46	0	0.8.0	213 P
M63573_at	11	2	20	20	18.055	2.70	0	0.5.5	213 P
U63541_al	11	2	20	20	18.055	1.87	0	0.5.5	213 P
U24105_al	9	0	20	20	18.045	1.85	0	0.1nf	212 P
M64992_at	10	1	20	20	17.050	2.15	1	0.10.0	210 P
U38846_al	12	1	20	20	18.060	1.89	0	0.12.0	209 P
U40282_al	11	3	20	20	18.055	1.59	0	0.3.7	208 P
M26576_c	7	2	20	20	18.035	1.40	0	0.3.5	207 P
S77812_at	9	2	20	20	18.045	1.80	0	0.4.5	206 P
U30825_at	10	2	20	20	17.050	2.18	0	0.5.0	206 P
M33552_al	9	1	20	20	18.045	1.19	0	0.9.0	205 P
U52112_m	9	1	20	20	18.045	1.97	1	0.9.0	205 P
M56503_at	12	2	20	20	17.060	2.77	2	0.6.0	202 P
S82240_at	12	1	20	20	18.060	3.55	2	0.12.0	201 P
M86528_at	7	1	20	20	18.035	1.20	0	0.7.0	200 P
M22632_at	9	1	20	20	18.045	1.38	0	0.9.0	199 P
M81601_al	11	2	20	20	18.055	1.77	0	0.5.5	199 P
M94556_al	12	1	20	20	18.080	2.15	0	0.12.0	199 P
M37435_al	7	1	20	20	18.035	1.74	0	0.7.0	197 P
M64098_at	11	2	20	20	18.055	2.31	0	0.5.5	197 P
U20998_at	8	2	20	20	18.040	2.68	1	0.4.0	196 P
U36764_at	14	1	20	20	17.070	3.29	0	0.14.0	196 P
U12255_al	8	1	20	20	18.040	1.73	0	0.8.0	195 P
U54778_at	8	1	20	20	18.040	1.23	0	0.8.0	195 P
M69039_at	14	2	20	20	17.070	2.86	0	0.7.0	194 P
M24502_at	11	0	20	20	18.055	2.34	0	0.1nf	183 P

Slide 4

Connective tissue B																			
U52100_at	12	0	20	20	18 0.60	2.09	0	0	0 Inf	192 P									
U03100_at	12	3	20	20	18 0.60	2.40	0	0	0 4.0	189 P									
M64347_at	10	2	20	20	18 0.50	1.08	0	0	0 5.0	186 P									
M61780_c	7	0	20	20	18 0.35	1.01	0	0	0 Inf	186 P									
M29877_at	10	1	20	20	18 0.50	1.51	0	0	1 10.0	181 P									
M62831_at	9	0	20	20	18 0.45	1.63	0	0	0 Inf	180 P									
U49785_at	12	0	20	20	18 0.60	1.76	1	1	0 Inf	178 P									
M31627_at	12	2	20	20	18 0.60	1.96	0	0	0 6.0	177 P									
U07424_at	10	3	20	20	18 0.50	1.50	0	0	0 3.3	177 P									
M89473_at	8	2	20	20	18 0.50	1.03	0	0	0 4.0	174 P									
U52101_at	7	1	20	20	18 0.35	1.22	0	0	0 7.0	174 P									
U16127_at	8	2	20	20	18 0.40	1.73	0	0	0 4.0	173 P									
U03686_at	10	2	20	20	18 0.60	2.96	0	0	0 5.0	172 P									
U57877_at	8	2	20	20	18 0.40	1.10	0	0	0 4.0	169 P									
M23114_at	14	1	20	20	17 0.70	2.87	1	1	0 14.0	167 P									
M73547_at	10	3	20	20	18 0.50	1.38	0	0	0 3.3	165 P									
U21049_at	7	0	20	20	18 0.35	0.95	0	0	0 Inf	165 P									
S67325_at	8	1	20	20	18 0.40	1.24	0	0	0 8.0	163 P									
U18009_at	10	2	20	20	18 0.50	1.86	0	0	0 5.0	163 P									
U50330_at	8	1	20	20	18 0.40	1.22	0	0	0 8.0	163 P									
U51878_at	12	2	20	20	18 0.60	1.84	0	0	0 6.0	160 P									
U24166_at	12	1	20	20	18 0.60	2.02	0	0	0 12.0	158 P									
U34962_at	10	2	20	20	18 0.50	1.26	0	0	0 5.0	152 P									
M57399_at	9	3	20	20	18 0.45	1.33	0	0	0 3.0	150 P									
U53476_at	7	1	20	20	18 0.35	1.13	0	0	0 7.0	150 P									
M24470_at	8	1	20	20	17 0.40	1.20	0	0	0 8.0	148 P									
M29927_at	8	0	20	20	17 0.40	1.33	0	0	0 Inf	147 P									
U51711_at	9	1	20	20	17 0.45	1.67	0	0	0 9.0	146 P									
M34057_at	10	3	20	20	18 0.50	2.37	1	1	0 3.3	145 P									
U43286_at	10	1	20	20	18 0.50	1.61	0	0	1 3.3	143 P									
S65583_m	14	3	20	20	17 0.70	3.30	1	1	0 14.0	143 P									
M86546_at	9	1	20	20	18 0.45	1.46	1	1	0 3.0	141 P									
U31384_at	10	1	20	20	17 0.50	1.83	1	1	0 10.0	140 P									
M63175_at	9	1	20	20	18 0.45	1.49	0	0	0 9.0	139 P									
M93283_at	10	2	20	20	18 0.40	1.48	0	0	0 4.0	138 P									
U30888_at	8	2	20	20	17 0.50	1.39	0	0	0 5.0	138 P									
U47101_at	9	0	20	20	18 0.40	1.54	0	0	0 4.0	138 P									
M97287_at	8	2	20	20	18 0.45	1.92	0	0	0 Inf	137 P									
AFX-M27	9	0	20	20	18 0.40	1.29	1	1	2 4.0	136 P									
U51240_at	7	1	20	20	18 0.45	2.11	0	0	0 Inf	136 P									
U49070_at	8	0	20	20	18 0.35	1.11	0	0	0 7.0	136 P									
M33195_at	9	1	20	20	18 0.45	1.08	0	0	0 Inf	135 P									
M59830_at	11	3	20	20	18 0.55	1.45	1	1	0 3.7	133 P									
U07802_at	10	2	20	20	17 0.50	1.85	0	0	0 5.0	133 P									
U39317_at	7	2	20	20	18 0.35	2.00	1	1	0 3.5	132 P									
U61374_at	9	1	20	20	18 0.45	1.43	0	0	0 9.0	132 P									
M88776_r	14	1	20	20	18 0.45	1.12	0	0	0 9.0	130 P									
M22877_at	7	1	20	20	17 0.70	2.26	1	1	0 14.0	129 P									
M91036_r	7	1	20	20	18 0.35	0.88	0	0	0 7.0	128 P									
S77763_at	9	2	20	20	18 0.45	1.34	0	0	0 4.5	126 P									
U58334_at	7	0	20	20	17 0.35	0.92	0	0	0 Inf	125 P									

Side 5

Connective tissue B																			
M64929_at	10	1	20	20	18 0.50	2.14	1	0	10.0	124 P									
S72008_at	10	0	20	20	17 0.50	2.43	1	0	Inf	124 P									
M35416_at	9	3	20	20	18 0.45	1.38	0	0	3.0	122 P									
M37721_at	12	3	20	20	18 0.60	2.38	1	0	4.0	122 P									
M55671_at	8	1	20	20	18 0.40	1.97	1	0	8.0	122 P									
M27492_at	8	1	20	20	18 0.45	1.71	1	0	9.0	121 P									
U52969_at	7	1	20	20	18 0.35	1.15	0	0	7.0	118 P									
M65542_at	13	2	20	20	18 0.65	3.06	3	0	6.5	117 P									
S81418_at	8	1	20	20	18 0.40	1.23	0	0	8.0	117 P									
U01147_at	8	1	20	20	18 0.40	1.42	0	0	8.0	116 P									
U10439_at	8	1	20	20	18 0.40	1.89	0	0	8.0	116 P									
M59916_at	8	2	20	20	18 0.40	1.19	0	0	4.0	115 P									
U24152_at	8	2	20	20	18 0.40	1.26	0	0	4.0	115 P									
M74524_at	7	0	20	20	18 0.35	2.07	1	0	Inf	114 P									
M83738_at	8	2	20	20	18 0.40	1.98	1	0	4.0	114 P									
S43646_at	7	2	20	20	18 0.35	1.31	0	0	3.5	114 P									
U0952_at	9	2	20	20	18 0.45	1.64	1	0	4.5	114 P									
U09770_at	8	1	20	20	17 0.40	1.08	0	0	8.0	114 P									
U15782_at	7	1	20	20	18 0.35	1.68	0	0	7.0	113 P									
U40368_at	9	1	20	20	18 0.45	1.88	1	0	8.0	113 P									
M23197_at	9	0	20	20	18 0.45	1.35	0	0	Inf	111 P									
U14193_at	8	2	20	20	17 0.40	1.13	0	0	4.0	109 P									
U37510_at	7	2	20	20	18 0.35	1.69	0	0	3.5	109 P									
U02082_at	11	0	20	20	18 0.55	1.54	0	0	Inf	108 P									
U47742_at	9	2	20	20	18 0.45	1.57	1	0	4.5	108 P									
J50553_at	8	0	20	20	18 0.40	1.20	0	0	Inf	106 P									
U25171_at	8	1	20	20	18 0.45	2.12	0	0	8.0	104 P									
M63603_at	10	2	20	20	17 0.40	1.16	0	0	8.0	103 P									
U07358_at	9	2	20	20	18 0.50	1.51	0	0	1.50	103 P									
U16031_at	9	3	20	20	18 0.45	1.51	1	0	4.5	103 P									
S83366_at	9	2	20	20	18 0.45	1.78	0	0	3.0	101 P									
M80482_at	7	1	20	20	18 0.45	1.34	0	0	4.5	100 P									
M96803_at	7	1	20	20	18 0.35	1.49	0	0	7.0	99 P									
S77415_at	9	2	20	20	18 0.45	2.53	2	0	4.5	95 P									
M30894_at	8	0	20	20	18 0.40	1.47	0	0	Inf	95 P									
S71018_at	7	0	20	20	18 0.35	1.12	0	0	Inf	95 P									
U13695_at	11	0	20	20	18 0.55	2.52	0	0	Inf	95 P									
U39400_at	10	3	20	20	18 0.50	1.81	0	0	3.3	94 P									
M77698_at	9	3	20	20	18 0.50	2.32	1	0	3.0	92 P									
U37251_at	10	1	20	20	18 0.45	1.45	1	0	10.0	91 P									
M90696_at	10	2	20	20	18 0.50	1.61	1	0	5.0	89 P									
U28386_at	9	3	20	20	18 0.45	1.71	3	0	1.30	88 P									
U08988_at	9	0	20	20	18 0.45	2.73	2	0	Inf	86 P									
S67156_at	8	0	20	20	18 0.40	1.84	0	0	Inf	85 P									
U28686_at	9	1	20	20	18 0.45	1.70	0	0	1.90	85 P									
U35046_at	10	1	20	20	17 0.50	2.17	1	0	10.0	83 P									
M30269_at	7	2	20	20	18 0.35	2.00	2	0	3.5	82 P									
M34308_at	9	3	20	20	18 0.45	1.72	1	0	3.0	82 P									
M37197_at	10	2	20	20	18 0.50	1.80	0	0	5.0	82 P									
U45976_at	11	1	20	20	18 0.55	2.70	0	0	11.0	80 P									
S80562_at	9	2	20	20	18 0.45	2.06	1	0	1.45	77 P									

Side 6

Connective tissue B									
U33818_at	9	1	20	20	18 0.45	0.99	0	1 9.0	77 P
M22995_at	9	0	20	20	18 0.45	1.52	0	0 Inf	76 P
U14747_at	8	2	20	20	18 0.40	1.09	0	0.40	76 P
M81118_at	9	3	20	20	18 0.45	1.52	2	1 3.0	75 P
M28983_at	7	2	20	20	18 0.35	1.30	1	0.35	74 P
M65217_at	9	3	20	20	18 0.45	2.24	2	0.30	72 P
M37825_at	10	3	20	20	18 0.50	1.50	0	0.33	70 P
M54992_at	10	3	20	20	18 0.50	1.38	0	0.33	70 P
U10117_at	9	3	20	20	18 0.45	1.52	1	0.30	70 P
U12471_at	7	2	20	20	18 0.35	1.55	0	0.35	70 P
U18242_at	9	2	20	20	18 0.45	2.09	0	0.45	70 P
U26032_at	9	3	20	20	18 0.45	1.63	1	0.30	70 P
M32886_at	10	2	20	20	17 0.50	0.94	0	0.50	66 P
U18291_at	9	2	20	20	18 0.45	2.26	1	0.45	66 P
S76965_at	8	2	20	20	18 0.40	1.70	2	0.40	65 P
U23070_at	9	3	20	20	18 0.45	1.44	2	0.30	65 P
M81378_at	7	1	20	20	18 0.35	1.05	0	0.70	63 P
U49436_at	10	2	20	20	18 0.50	2.41	2	0.50	63 P
M25393_at	9	3	20	20	18 0.45	1.61	1	1 3.0	62 P
M86579_at	9	3	20	20	18 0.45	1.74	2	0.30	62 P
M62397_at	9	2	20	20	18 0.45	1.92	1	0.45	60 P
M63623_at	7	2	20	20	18 0.35	1.40	0	0.35	57 P
U23942_at	7	0	20	20	18 0.35	1.40	0	0 Inf	56 P
U18062_at	8	1	20	20	18 0.40	1.83	1	0.80	50 P
S67788_at	8	2	20	20	18 0.40	1.33	0	0.40	49 P
M74093_at	8	2	20	20	18 0.40	1.09	0	0.40	48 P
U00951_at	8	2	20	20	18 0.40	1.61	1	0.40	47 P
U50939_at	7	2	20	20	18 0.35	1.47	1	0.35	46 P
U24576_at	8	2	20	20	18 0.40	2.15	1	0.40	42 P
U07151_at	8	2	20	20	18 0.40	1.14	0	0.40	40 P
U38810_at	8	1	20	20	18 0.40	1.37	1	0.80	40 P
U13948_at	9	2	20	20	18 0.45	1.61	1	0.45	37 P
S78569_at	7	1	20	20	18 0.35	0.89	0	0.70	35 P
U28833_at	7	1	20	20	18 0.35	1.04	0	1 7.0	33 P
U29615_at	8	2	20	20	18 0.40	1.05	0	0.40	33 P
M81882_at	8	2	20	20	18 0.40	1.65	1	0.40	31 P
U57452_at	7	1	20	20	18 0.35	0.96	0	0 7.0	29 P

Gene Name	Connective tissue C																								
	Posit	Negat	Painr	Painr	Painr	In	Pos	Fractl	Log Avg	PM	Ex	MM	Excess	Pos/Neg	Avg Diff	Abs Call									
Z23090_at	20	0	20	20	20	18	1.00	6.28	1	0	Inf	0	Inf	9609 P											
Z70758_at	20	0	20	20	20	18	1.00	8.75	11	0	Inf	0	Inf	7648 P											
Z12962_at	18	0	20	20	20	18	0.90	6.95	3	0	Inf	0	Inf	7468 P											
X07695_at	20	0	20	20	20	18	1.00	6.77	2	0	Inf	0	Inf	7458 P											
hum_ali_at	69	0	69	69	69	67	1.00	7.07	11	0	Inf	0	Inf	7071 P											
X69150_at	19	0	20	20	20	18	0.95	7.89	8	0	Inf	0	Inf	8256 P											
X17206_at	20	0	20	20	20	18	1.00	7.81	8	0	Inf	0	Inf	4928 P											
X16084_at	19	0	20	20	20	18	0.95	8.14	6	0	Inf	0	Inf	4572 P											
X56932_at	20	0	20	20	20	18	1.00	7.69	5	0	Inf	0	Inf	4210 P											
AFFX-HUMGAPDH/M33197_3_at	20	0	20	20	20	18	1.00	7.15	2	0	Inf	0	Inf	4188 P											
AFFX-HSAC07/X00351_M_at	20	0	20	20	20	18	1.00	6.52	1	0	Inf	0	Inf	3970 P											
X00822_at	19	0	20	20	20	18	0.95	6.50	1	0	Inf	0	Inf	3963 P											
X03342_at	20	0	20	20	20	18	1.00	7.76	5	0	Inf	0	Inf	3818 P											
X67247_ma1_at	20	0	20	20	20	18	1.00	8.34	6	0	Inf	0	Inf	3725 P											
X08617_at	20	0	20	20	20	18	1.00	6.38	2	0	Inf	0	Inf	3387 P											
X15940_at	19	0	20	20	20	18	0.95	7.29	5	0	Inf	0	Inf	3375 P											
X63527_at	19	0	20	20	20	18	0.95	7.71	7	0	Inf	0	Inf	3282 P											
X05908_at	19	0	20	20	20	18	0.95	8.70	8	0	Inf	0	Inf	3217 P											
AFFX-CreX-3_at	19	0	20	20	20	18	0.95	8.12	6	0	Inf	0	Inf	3155 P											
AFFX-HSAC07/X00351_3_at	20	0	20	20	20	18	1.00	6.57	2	0	Inf	0	Inf	2894 P											
X73460_at	19	0	20	20	20	18	0.95	6.62	3	0	Inf	0	Inf	2849 P											
X62691_at	20	0	20	20	20	18	1.00	7.33	4	0	Inf	0	Inf	2885 P											
AFFX-HSAC07/X00351_5_at	19	0	20	20	20	18	0.95	6.46	1	0	Inf	0	Inf	2782 P											
X00274_at	20	0	20	20	20	18	1.00	7.97	8	0	Inf	0	Inf	2780 P											
AFFX-HUMGAPDH/M33197_M_at	18	0	20	20	20	18	0.90	5.92	0	0	Inf	0	Inf	2639 P											
X79234_at	20	0	20	20	20	18	1.00	8.10	4	0	Inf	0	Inf	2602 P											
X55954_at	20	0	20	20	20	18	1.00	7.53	6	0	Inf	0	Inf	2495 P											
Z26876_at	20	0	20	20	20	18	0.85	7.65	6	0	Inf	0	Inf	2490 P											
Z28407_at	17	0	20	20	20	18	0.95	5.59	1	0	Inf	0	Inf	2386 P											
Y07755_at	18	0	20	20	20	18	0.95	7.10	2	0	Inf	0	Inf	2378 P											
X64707_at	19	0	20	20	20	18	0.95	5.87	2	0	Inf	0	Inf	2268 P											
AFFX-CreX-5_at	19	0	20	20	20	18	0.95	7.77	3	0	Inf	0	Inf	2185 P											
U78027_ma3_at	18	2	20	20	20	18	0.90	7.38	6	0	Inf	0	Inf	2156 P											
X67683_at	18	0	20	20	20	18	0.95	5.62	1	0	Inf	0	Inf	2126 P											
AFFX-HUMGAPDH/M33197_5_at	19	0	20	20	20	18	0.95	7.18	6	0	Inf	0	Inf	2120 P											
X69391_at	18	0	20	20	20	18	0.95	7.24	4	0	Inf	0	Inf	2084 P											
AB002533_at	18	0	20	20	20	18	0.95	5.92	0	0	Inf	0	Inf	2063 P											
X68277_at	19	0	20	20	20	18	0.95	8.28	7	0	Inf	0	Inf	1972 P											
X53777_at	18	1	20	20	20	18	0.90	7.13	6	0	Inf	0	Inf	1915 P											
X55715_at	20	0	20	20	20	18	1.00	7.32	2	0	Inf	0	Inf	1744 P											
X52851_ma1_at	20	0	20	20	20	18	1.00	6.55	3	0	Inf	0	Inf	1727 P											
X67951_at	20	0	20	20	20	18	1.00	6.97	2	0	Inf	0	Inf	1472 P											
X77584_at	19	0	20	20	20	18	0.95	7.09	3	0	Inf	0	Inf	1470 P											
X02152_at	18	0	20	20	20	18	0.90	6.79	2	0	Inf	0	Inf	1432 P											
X57959_at	19	0	20	20	20	18	0.95	7.24	3	0	Inf	0	Inf	1426 P											
X13839_at	18	0	20	20	20	18	0.90	6.61	3	0	Inf	0	Inf	1405 P											
AFFX-BioDr-3_at	17	2	20	20	20	18	0.85	4.13	0	0	Inf	0	Inf	1401 P											
X52966_at	17	1	20	20	20	18	0.85	6.56	5	0	Inf	0	Inf	1381 P											
X15341_at	20	0	20	20	20	18	1.00	6.81	6	0	Inf	0	Inf	1338 P											
X56997_ma1_at	17	0	20	20	20	18	0.85	5.20	2	0	Inf	0	Inf	1308 P											

Slide 1

57

Connective tissue C										
X60908_at	18	0	20	20	18 0.90	7.15	4	0	Inf	1203 P
X60489_at	19	0	20	20	18 0.95	6.91	4	0	Inf	1168 P
X12447_at	15	0	20	20	18 0.75	3.29	1	0	Inf	1127 P
Z225749_ma1_at	18	1	20	20	18 0.90	5.26	0	0	18.0	1122 P
X51466_at	18	0	20	20	18 0.80	5.14	1	0	Inf	1116 P
X53331_at	18	0	20	20	18 0.90	6.29	1	0	Inf	1079 P
Z19574_ma1_at	19	0	20	20	18 0.95	5.04	0	0	Inf	1059 P
X82593_at	19	0	20	20	18 0.95	4.56	0	0	Inf	1046 P
X95404_at	15	0	20	20	18 0.75	4.66	1	0	Inf	960 P
AF001548_ma1_at	17	0	20	20	18 0.85	5.12	1	0	Inf	950 P
X15183_at	17	1	20	20	18 0.85	6.82	2	0	17.0	918 P
U94586_at	20	0	20	20	17 1.00	8.01	6	0	Inf	876 P
X16560_at	17	0	20	20	18 0.85	6.16	3	0	Inf	858 P
U65932_at	19	0	20	20	18 0.95	5.61	0	0	Inf	853 P
X07686_at	17	0	20	20	18 0.85	5.86	1	0	Inf	777 P
X15822_at	18	0	20	20	18 0.90	5.06	3	0	Inf	760 P
V00572_at	20	0	20	20	18 1.00	6.57	2	0	Inf	758 P
X04412_at	17	1	20	20	18 0.85	4.49	1	0	17.0	746 P
X93036_at	16	0	20	20	17 0.80	4.59	1	0	Inf	730 P
Y00433_at	17	0	20	20	18 0.85	4.30	0	0	Inf	708 P
X65614_at	18	0	20	20	18 0.90	5.02	1	0	Inf	687 P
U90815_at	18	1	20	20	18 0.90	5.53	3	0	18.0	684 P
X16832_at	16	0	20	20	18 0.80	4.30	0	0	Inf	661 P
X05276_at	19	0	20	20	18 0.95	4.58	0	0	Inf	642 P
AFFX-HSAC07/X00351_3_at	18	0	20	20	18 0.90	4.98	0	0	Inf	630 P
U73824_at	18	0	20	20	18 0.95	6.59	3	0	Inf	586 P
V01612_ma1_at	19	0	20	20	18 0.95	6.39	2	0	Inf	574 P
U93205_at	18	0	20	20	18 0.90	3.74	0	0	Inf	570 P
X13238_at	17	1	20	20	18 0.85	5.69	1	0	17.0	563 P
X56494_at	14	1	20	20	18 0.70	3.58	1	0	14.0	563 P
X07979_at	18	1	20	20	17 0.90	5.96	2	0	18.0	543 P
X86693_at	18	0	20	20	18 0.80	5.33	2	0	Inf	533 P
Z48950_at	17	0	20	20	18 0.85	4.43	0	0	Inf	527 P
X02317_at	18	0	20	20	18 0.95	5.45	0	0	Inf	509 P
X59634_at	17	1	20	20	18 0.85	5.44	0	0	17.0	482 P
Z24727_at	17	0	20	20	18 0.85	5.17	2	0	Inf	464 P
X56468_at	18	0	20	20	18 0.90	5.18	1	0	Inf	462 P
X03100_cd82_at	14	0	20	20	18 0.70	3.39	1	0	Inf	457 P
Y00503_at	18	0	20	20	18 0.90	4.44	0	0	Inf	452 P
U67171_at	12	0	20	20	18 0.60	2.64	0	0	Inf	440 P
U78095_at	16	1	20	20	17 0.80	3.28	0	0	16.0	435 P
X15880_at	10	1	20	20	18 0.50	3.08	0	0	10.0	429 P
X69550_at	13	1	20	20	18 0.65	2.30	0	0	13.0	420 P
X62654_ma1_at	17	1	20	20	17 0.85	3.73	1	0	17.0	404 P
X57698_at	17	0	20	20	18 0.85	3.49	0	0	Inf	401 P
U72511_at	15	0	20	20	18 0.75	3.49	1	0	Inf	383 P
X04108_at	13	2	20	20	18 0.65	2.50	0	0	6.5	393 P
X68314_at	14	0	20	20	18 0.70	3.09	0	0	Inf	380 P
X51521_at	18	1	20	20	18 0.95	4.60	1	0	19.0	376 P
X60036_at	17	0	20	20	18 0.85	4.60	0	0	Inf	376 P
U78284_at	15	1	20	20	18 0.75	3.95	2	0	15.0	370 P
X59892_at	12	1	20	20	18 0.60	2.57	0	0	12.0	366 P

Connective tissue C									
U70370_at	12	2	20	20	18.060	2.66	1	0.60	361 P
X91504_at	11	1	20	20	18.055	1.54	0	0.11.0	360 P
U73843_at	13	1	20	20	18.065	3.39	1	0.13.0	356 P
L20888_at	13	0	20	20	18.065	2.63	0	0 Inf	356 P
X16662_at	14	2	20	20	18.070	3.64	1	0.7.0	355 P
X54304_at	15	0	20	20	18.075	3.90	0	0 Inf	350 P
Y00764_at	17	1	20	20	18.085	5.54	2	0.17.0	347 P
Z29505_at	18	0	20	20	18.090	4.62	0	0 Inf	345 P
U90878_at	16	1	20	20	18.080	5.35	0	0.16.0	335 P
Z21507_at	15	1	20	20	18.075	4.28	0	0.15.0	335 P
Z32765_at	11	1	20	20	18.055	2.00	0	0.11.0	330 P
X60221_at	17	1	20	20	18.085	5.00	0	0.17.0	329 P
X62320_at	10	0	20	20	18.050	2.31	0	0 Inf	327 P
X83218_at	17	0	20	20	18.085	5.28	0	0 Inf	322 P
X52003_at	9	2	20	20	18.045	2.33	0	0.4.5	321 P
X15882_at	11	2	20	20	18.055	1.84	0	0.5.5	314 P
X17042_at	16	0	20	20	17.080	5.83	3	0 Inf	314 P
X78136_at	15	1	20	20	18.075	4.66	0	0.15.0	309 P
Y00486_rna1_at	8	0	20	20	18.040	1.74	0	0 Inf	307 P
X13794_rna1_at	16	1	20	20	18.080	4.91	1	0.16.0	300 P
U70735_at	17	0	20	20	18.085	3.57	0	0 Inf	288 P
X71973_at	12	1	20	20	18.060	2.30	0	0.12.0	287 P
U78521_at	8	0	20	20	18.045	1.26	0	0 Inf	296 P
U94855_at	18	0	20	20	18.090	4.74	0	0 Inf	293 P
D29805_at	11	3	20	20	18.055	2.57	1	0.3.7	291 P
X75851_at	16	1	20	20	18.080	4.65	1	0.16.0	290 P
AFFX-BioDr-5_at	13	0	20	20	18.065	3.14	0	0 Inf	288 P
U77604_at	13	0	20	20	18.085	2.79	0	0.13.0	286 P
X90858_at	15	2	20	20	18.075	3.54	0	0.7.5	285 P
X86809_at	11	1	20	20	18.055	1.89	0	0.11.0	283 P
X80692_at	14	0	20	20	18.070	3.84	0	0 Inf	276 P
U72512_at	7	0	20	20	17.035	1.41	0	0 Inf	272 P
X55733_at	14	0	20	20	18.070	3.92	2	0 Inf	272 P
Y00281_at	14	2	20	20	18.070	3.22	0	0.7.0	272 P
U80313_at	17	0	20	20	18.085	3.78	0	0 Inf	270 P
X81817_at	15	2	20	20	18.075	3.43	1	0.7.5	266 P
Z48199_at	10	1	20	20	18.050	1.74	0	0.10.0	263 P
U77504_at	10	0	20	20	18.050	2.03	0	0 Inf	262 P
X75593_at	10	2	20	20	18.050	2.92	1	0.5.0	260 P
Z14244_at	18	0	20	20	17.090	6.43	5	0 Inf	260 P
X91247_at	18	1	20	20	18.090	4.44	0	0.18.0	258 P
X06985_at	11	1	20	20	18.055	2.03	1	0.11.0	257 P
X76180_at	12	1	20	20	18.060	2.72	0	0.12.0	255 P
X76717_at	10	1	20	20	18.050	2.26	0	0.10.0	251 P
U65785_at	11	0	20	20	18.055	1.75	0	0 Inf	249 P
X91257_at	13	0	20	20	18.065	3.06	0	0 Inf	249 P
X87836_at	16	0	20	20	18.080	4.72	1	0 Inf	248 P
X75252_at	12	1	20	20	18.060	3.02	0	0.12.0	247 P
X97074_at	12	0	20	20	18.060	2.12	0	0 Inf	247 P
X16135_at	14	2	20	20	18.070	3.23	0	0.7.0	242 P
X99688_at	8	1	20	20	18.045	1.72	0	0.9.0	242 P
U34569_at	13	2	20	20	17.065	1.94	0	0.6.5	241 P

Side 3

Connective tissue C									
X13444_at	9	0	20	20	18.045	1.61	0	0 Inf	241 P
U70732_ma1_at	9	2	20	20	18.045	1.35	0	0 4.5	240 P
X71428_at	11	1	20	20	18.055	2.25	0	0 11.0	240 P
U83115_at	13	0	20	20	18.065	3.05	1	0 Inf	239 P
X82434_at	11	0	20	20	18.055	1.84	0	0 Inf	237 P
X59417_at	14	2	20	20	18.070	2.91	1	1 7.0	231 P
X57346_at	13	1	20	20	17.065	3.80	0	0 13.0	230 P
X85785_ma1_at	9	0	20	20	18.045	1.61	0	0 Inf	229 P
X13546_ma1_at	15	0	20	20	17.075	2.97	0	0 Inf	222 P
X52730_ma1_at	8	0	20	20	18.040	1.24	0	0 Inf	222 P
X74104_at	15	1	20	20	18.075	4.00	1	0 15.0	222 P
U68878_at	9	2	20	20	17.045	2.00	0	0 4.5	221 P
Z27113_at	11	1	20	20	18.055	2.14	0	0 11.0	221 P
U66059_cds7_at	10	1	20	20	18.050	1.73	0	0 10.0	220 P
D13146_cds1_at	7	0	20	20	18.035	1.70	0	0 Inf	218 P
AFFX-BioC-5_at	16	0	20	20	18.080	3.02	0	0 Inf	217 P
X89910_at	15	1	20	20	18.075	3.67	0	0 15.0	217 P
U78678_at	9	1	20	20	18.045	1.58	0	0 9.0	215 P
X76013_at	11	1	20	20	18.055	2.70	0	0 11.0	215 P
U70867_at	9	1	20	20	18.045	1.44	0	0 9.0	212 P
X69433_at	9	1	20	20	18.045	2.12	0	0 9.0	212 P
X86924_ma1_at	7	1	20	20	18.035	1.37	0	0 7.0	209 P
U77827_at	8	0	20	20	18.045	1.98	1	0 Inf	208 P
X89908_ma1_at	9	2	20	20	18.045	2.00	1	0 4.5	209 P
X80200_at	10	1	20	20	17.050	2.04	0	0 10.0	208 P
Z11793_at	15	1	20	20	18.075	4.49	4	0 15.0	208 P
U81556_at	12	2	20	20	18.060	2.25	0	0 6.0	207 P
U67983_at	9	1	20	20	18.045	2.10	0	0 9.0	206 P
X89585_at	14	1	20	20	18.070	4.48	1	0 14.0	206 P
U68566_at	10	2	20	20	18.050	1.94	0	0 5.0	204 P
U77398_at	8	0	20	20	18.040	1.53	0	0 Inf	201 P
U88629_at	12	1	20	20	18.060	3.30	0	0 12.0	199 P
X02612_at	12	1	20	20	18.080	2.99	0	0 12.0	199 P
X15187_at	14	1	20	20	18.070	3.68	0	0 14.0	188 P
Y00282_at	14	0	20	20	18.070	3.70	1	0 Inf	199 P
U85611_at	11	1	20	20	18.055	2.16	0	0 11.0	192 P
X72964_at	12	0	20	20	18.050	2.74	0	0 Inf	192 P
U73379_at	12	0	20	20	17.080	1.94	0	0 Inf	191 P
X56263_ma1_at	12	1	20	20	18.060	2.65	1	0 12.0	191 P
X64559_at	10	1	20	20	18.050	1.50	0	0 10.0	190 P
U86529_at	7	0	20	20	18.035	1.58	0	0 Inf	189 P
X04368_at	11	1	20	20	18.055	2.47	0	0 11.0	188 P
X52947_at	14	0	20	20	18.070	5.43	2	0 Inf	188 P
U70663_at	8	0	20	20	18.040	1.58	0	0 Inf	187 P
X89750_at	18	0	20	20	18.085	4.23	0	0 Inf	186 P
Y08976_at	9	1	20	20	18.045	1.58	0	0 9.0	185 P
X69689_at	7	0	20	20	18.035	1.59	0	0 Inf	183 P
X01388_at	7	1	20	20	18.035	1.02	0	0 7.0	182 P
U70063_at	9	3	20	20	18.045	2.13	0	0 3.0	176 P
U72517_at	10	2	20	20	18.050	1.56	0	0 5.0	175 P
X76228_at	11	1	20	20	18.055	2.50	0	0 11.0	175 P
X78549_at	13	0	20	20	17.065	1.73	1	0 Inf	175 P

Connective tissue C																			
Z14000_at	7	0	20	20	18 0.35	1.05	0	0	0	0	0	0	0	0	0	0	0	0	174 P
U79254_at	13	1	20	20	18 0.65	4.22	0	0	0	0	0	0	0	0	0	0	0	0	165 P
X62078_at	9	0	20	20	18 0.45	1.84	0	0	0	0	0	0	0	0	0	0	0	0	165 P
U94585_at	10	3	20	20	18 0.50	1.40	0	0	0	0	0	0	0	0	0	0	0	0	163 P
U72066_at	11	1	20	20	18 0.55	1.50	0	0	0	0	0	0	0	0	0	0	0	0	162 P
U88964_at	9	1	20	20	18 0.45	2.60	0	0	0	0	0	0	0	0	0	0	0	0	161 P
U70660_at	9	1	20	20	18 0.45	1.35	0	0	0	0	0	0	0	0	0	0	0	0	160 P
X52541_at	16	0	20	20	17 0.80	3.99	2	0	0	0	0	0	0	0	0	0	0	0	160 P
X95586_at	16	0	20	20	18 0.80	3.20	0	0	0	0	0	0	0	0	0	0	0	0	160 P
X71129_at	10	1	20	20	17 0.50	1.88	1	0	0	0	0	0	0	0	0	0	0	0	159 P
X53416_at	8	0	20	20	18 0.40	1.85	0	0	0	0	0	0	0	0	0	0	0	0	158 P
X12794_at	8	1	20	20	18 0.40	1.58	0	0	0	0	0	0	0	0	0	0	0	0	157 P
X61970_at	13	0	20	20	18 0.65	3.44	0	0	0	0	0	0	0	0	0	0	0	0	157 P
Z37986_at	9	1	20	20	18 0.45	1.81	0	0	0	0	0	0	0	0	0	0	0	0	157 P
J04182_at	12	1	20	20	18 0.60	2.60	0	0	0	0	0	0	0	0	0	0	0	0	157 P
AFFX-BioC-3_at	11	1	20	20	18 0.55	2.12	0	0	0	0	0	0	0	0	0	0	0	0	156 P
X14787_at	12	2	20	20	18 0.60	4.02	0	0	0	0	0	0	0	0	0	0	0	0	155 P
X62535_at	10	0	20	20	18 0.50	2.78	1	0	0	0	0	0	0	0	0	0	0	0	155 P
X85373_at	11	0	20	20	18 0.55	2.75	1	0	0	0	0	0	0	0	0	0	0	0	155 P
X98484_at	10	1	20	20	18 0.50	1.71	0	0	0	0	0	0	0	0	0	0	0	0	154 P
X98311_at	9	0	20	20	18 0.45	1.80	0	0	0	0	0	0	0	0	0	0	0	0	154 P
L00205_at	12	0	20	20	18 0.60	2.47	0	0	0	0	0	0	0	0	0	0	0	0	154 P
X16316_at	10	2	20	20	18 0.50	1.87	0	0	0	0	0	0	0	0	0	0	0	0	153 P
U69263_at	14	1	20	20	17 0.70	2.22	0	0	0	0	0	0	0	0	0	0	0	0	152 P
X74801_at	11	0	20	20	18 0.55	3.34	0	0	0	0	0	0	0	0	0	0	0	0	152 P
U70322_at	13	1	20	20	18 0.65	2.19	0	0	0	0	0	0	0	0	0	0	0	0	151 P
D88988_at	7	0	20	20	18 0.35	1.09	0	0	0	0	0	0	0	0	0	0	0	0	151 P
V00563_at	11	1	20	20	18 0.55	2.59	1	0	0	0	0	0	0	0	0	0	0	0	150 P
X76029_at	7	2	20	20	18 0.35	1.35	0	0	0	0	0	0	0	0	0	0	0	0	150 P
U78798_at	9	3	20	20	18 0.45	1.83	0	0	0	0	0	0	0	0	0	0	0	0	148 P
X90872_at	12	2	20	20	18 0.60	1.80	0	0	0	0	0	0	0	0	0	0	0	0	148 P
U78524_at	7	1	20	20	18 0.35	1.34	1	0	0	0	0	0	0	0	0	0	0	0	147 P
X04500_at	9	2	20	20	17 0.45	1.39	0	0	0	0	0	0	0	0	0	0	0	0	147 P
X12791_at	12	1	20	20	18 0.60	2.05	0	0	0	0	0	0	0	0	0	0	0	0	146 P
X80199_at	12	1	20	20	18 0.60	2.67	0	0	0	0	0	0	0	0	0	0	0	0	146 P
X83425_at	9	2	20	20	18 0.45	1.76	0	0	0	0	0	0	0	0	0	0	0	0	146 P
X13867_at	9	2	20	20	18 0.45	1.96	0	0	0	0	0	0	0	0	0	0	0	0	145 P
X83422_at	9	2	20	20	17 0.45	2.55	0	0	0	0	0	0	0	0	0	0	0	0	145 P
X74008_at	9	3	20	20	18 0.45	2.32	1	0	0	0	0	0	0	0	0	0	0	0	145 P
X99920_at	12	1	20	20	18 0.60	2.85	1	0	0	0	0	0	0	0	0	0	0	0	145 P
Z50022_at	12	0	20	20	18 0.60	1.68	0	0	0	0	0	0	0	0	0	0	0	0	143 P
X74795_at	11	3	20	20	17 0.55	2.46	0	0	0	0	0	0	0	0	0	0	0	0	143 P
X68733_ma1_at	8	0	20	20	18 0.40	1.30	0	0	0	0	0	0	0	0	0	0	0	0	142 P
X76534_at	15	0	20	20	17 0.75	4.86	1	0	0	0	0	0	0	0	0	0	0	0	142 P
X82456_at	15	0	20	20	18 0.75	3.78	1	0	0	0	0	0	0	0	0	0	0	0	142 P
Z47727_at	12	0	20	20	18 0.60	2.81	0	0	0	0	0	0	0	0	0	0	0	0	142 P
U82010_ma1_at	12	0	20	20	18 0.80	2.54	1	0	0	0	0	0	0	0	0	0	0	0	141 P
U70451_at	7	1	20	20	18 0.35	1.19	0	0	0	0	0	0	0	0	0	0	0	0	139 P
X17620_at	8	2	20	20	18 0.40	1.31	0	0	0	0	0	0	0	0	0	0	0	0	139 P
X76770_at	13	1	20	20	18 0.65	3.07	0	0	0	0	0	0	0	0	0	0	0	0	139 P
AFFX-HUMPMGE/M10098_5_at	10	2	20	20	18 0.50	2.39	0	0	0	0	0	0	0	0	0	0	0	0	139 P
U88063_at	14	0	20	20	18 0.70	3.15	0	0	0	0	0	0	0	0	0	0	0	0	137 P

Side 5

Connective tissue C									
U77948_at	14	0	20	20	18 0.70	3.86	0	0 Inf	137 P
D50405_at	11	1	20	20	18 0.55	1.94	0	0 11.0	137 P
HG651-HT4201_at	7	0	20	20	18 0.35	1.44	0	0 Inf	136 P
U89336_cds3_at	10	0	20	20	18 0.50	1.83	0	0 Inf	134 P
X76342_at	13	2	20	20	18 0.65	2.84	0	0 6.5	132 P
X54232_at	10	1	20	20	17 0.50	1.70	0	0 10.0	131 P
X70476_at	12	0	20	20	17 0.60	2.84	1	0 Inf	131 P
U68488_at	9	1	20	20	18 0.45	1.34	0	0 9.0	130 P
X01060_at	14	2	20	20	18 0.70	2.96	0	0 7.0	130 P
X14675_at	8	0	20	20	18 0.45	1.41	0	0 Inf	130 P
Y10032_at	14	4	20	20	18 0.70	2.96	3	1 3.5	130 P
D16105_at	8	1	20	20	18 0.40	1.31	0	0 8.0	130 P
U86070_at	11	3	20	20	18 0.55	1.48	0	0 3.7	128 P
Z24725_at	15	0	20	20	18 0.75	4.60	2	0 Inf	128 P
X52882_at	11	0	20	20	18 0.55	2.22	0	0 Inf	127 P
L00056_at	10	0	20	20	18 0.50	2.95	1	0 Inf	127 P
U86915_at	10	1	20	20	18 0.50	1.94	0	0 10.0	126 P
X64364_at	7	0	20	20	17 0.35	1.30	0	0 Inf	126 P
X86779_at	7	0	20	20	17 0.35	1.19	0	0 Inf	125 P
Z84721_cds2_at	12	4	20	20	18 0.60	1.58	0	0 3.0	125 P
X03656_ma1_at	10	2	20	20	17 0.50	1.82	1	0 5.0	124 P
X82895_at	9	1	20	20	18 0.45	1.91	0	0 9.0	124 P
Y09616_at	12	2	20	20	17 0.60	2.08	0	0 6.0	121 P
U67784_at	10	1	20	20	18 0.50	1.97	0	0 10.0	120 P
U80040_at	11	2	20	20	18 0.55	1.66	0	0 5.5	120 P
X72755_at	16	2	20	20	17 0.80	3.68	0	0 8.0	120 P
X60592_at	10	2	20	20	18 0.50	1.12	0	0 5.0	118 P
AFFX-HUMISGF3A/M97935_3_at	12	1	20	20	18 0.60	3.01	2	0 12.0	118 P
U78793_at	10	2	20	20	17 0.50	2.45	0	0 5.0	118 P
X12451_at	12	0	20	20	18 0.60	3.43	2	0 Inf	118 P
X75342_at	11	2	20	20	17 0.55	1.51	0	0 5.5	117 P
X01630_at	10	1	20	20	18 0.50	2.24	1	0 10.0	114 P
X82153_at	13	0	20	20	18 0.65	2.42	0	0 Inf	114 P
L11066_at	7	1	20	20	18 0.35	0.93	0	0 7.0	114 P
U90426_at	12	0	20	20	18 0.60	3.55	1	0 Inf	113 P
U91932_at	11	1	20	20	17 0.55	2.45	0	0 11.0	113 P
X92098_at	10	0	20	20	18 0.50	2.12	0	0 Inf	113 P
Y08134_at	8	1	20	20	18 0.40	1.74	0	0 8.0	113 P
U79260_at	7	0	20	20	18 0.35	1.62	0	0 Inf	112 P
U88336_cds1_at	10	1	20	20	18 0.50	2.01	0	0 10.0	112 P
X05409_at	7	1	20	20	18 0.35	1.29	0	0 7.0	112 P
X95735_at	10	1	20	20	18 0.50	1.85	1	0 10.0	112 P
Y11681_at	8	1	20	20	18 0.40	1.40	0	0 8.0	112 P
U97105_at	12	0	20	20	18 0.60	2.89	0	0 Inf	111 P
X03934_at	10	0	20	20	17 0.50	1.55	0	0 Inf	111 P
X61123_at	14	0	20	20	17 0.70	4.15	2	0 Inf	111 P
X73113_at	9	2	20	20	18 0.45	1.12	0	0 4.5	111 P
X86163_at	11	1	20	20	18 0.55	2.44	0	0 11.0	111 P
U79267_at	14	0	20	20	17 0.70	2.31	0	0 Inf	110 P
X15414_at	10	0	20	20	17 0.50	1.76	0	0 Inf	110 P
U82671_cds2_at	8	0	20	20	18 0.40	1.72	0	0 Inf	109 P
X99728_at	9	2	20	20	18 0.45	1.44	0	0 4.5	109 P

Side 6

Connective tissue C

L10413_at	12	1	20	20	18.60	1.98	0	0	0.12.0	109 P
U78262_at	10	3	20	20	18.50	1.67	0	0	0.3.3	106 P
U78556_at	11	1	20	20	18.55	2.08	0	0	0.11.0	104 P
Z50194_at	12	2	20	20	18.60	2.75	1	0	0.6.0	103 P
X16416_at	7	1	20	20	18.35	1.51	0	0	0.7.0	102 P
X70340_at	7	0	20	20	18.35	1.68	0	0	0.1nf	101 P
Y00815_at	12	0	20	20	18.60	2.85	1	0	0.1nf	101 P
X62744_at	7	2	20	20	18.35	1.34	0	0	0.3.5	100 P
X65873_at	12	3	20	20	18.60	2.43	1	0	0.4.0	100 P
X02530_at	9	1	20	20	18.45	2.34	0	0	0.9.0	99 P
X71874_cdsl_at	8	1	20	20	18.40	1.24	0	0	0.8.0	99 P
U90913_at	9	0	20	20	18.45	1.97	0	0	0.1nf	98 P
Z35093_at	9	1	20	20	18.45	1.74	0	0	0.8.0	98 P
Z36531_at	13	2	20	20	18.65	2.63	0	0	0.6.5	98 P
Z48042_at	10	1	20	20	18.50	1.45	0	0	0.10.0	98 P
X62200_at	10	2	20	20	18.50	2.28	0	0	0.5.0	97 P
X06323_at	16	0	20	20	18.80	3.63	0	0	0.1nf	96 P
X52151_at	9	1	20	20	18.45	1.37	0	0	0.9.0	96 P
U83463_at	12	1	20	20	17.60	3.70	2	0	0.12.0	95 P
X93499_at	10	1	20	20	17.50	2.14	0	0	0.11.0	95 P
HG2743-HT2845_at	10	1	20	20	17.50	2.62	2	0	0.10.0	95 P
X74295_at	9	1	20	20	18.45	0.94	0	0	0.9.0	94 P
X80695_at	9	2	20	20	18.45	1.32	0	0	0.4.5	94 P
X92744_at	9	0	20	20	17.45	1.72	0	0	0.1nf	94 P
Z47087_at	14	1	20	20	17.70	3.25	0	0	0.14.0	94 P
U86782_at	14	0	20	20	18.00	3.19	0	0	0.1nf	93 P
X77794_at	14	1	20	20	17.70	3.63	1	0	0.14.0	93 P
U89278_at	8	2	20	20	18.40	0.85	0	0	0.4.0	91 P
X78732_at	13	0	20	20	18.65	3.90	0	0	0.1nf	91 P
X80810_at	10	0	20	20	18.50	2.51	0	0	0.1nf	91 P
U81802_at	7	1	20	20	18.35	1.52	0	0	0.7.0	90 P
X66401_cds1_at	12	1	20	20	18.60	2.65	0	0	0.12.0	90 P
X97302_at	8	0	20	20	17.40	1.60	0	0	0.1nf	89 P
X54942_at	11	1	20	20	18.55	2.13	1	0	0.11.0	89 P
X62466_at	8	2	20	20	17.40	2.09	0	0	0.4.0	89 P
X76104_at	7	2	20	20	18.35	1.34	0	0	0.3.5	89 P
X81003_at	11	0	20	20	18.55	2.07	0	0	0.1nf	89 P
U79287_at	13	0	20	20	17.65	2.37	0	0	0.1nf	88 P
U86502_at	8	0	20	20	18.40	1.56	0	0	0.1nf	88 P
X57766_at	8	1	20	20	18.45	1.57	0	0	0.8.0	88 P
Y08989_at	9	2	20	20	18.60	1.69	1	0	0.4.5	88 P
U72209_at	12	2	20	20	18.60	2.04	2	0	0.6.0	87 P
X85372_at	9	2	20	20	17.45	1.32	1	0	0.4.5	87 P
Y08915_at	11	1	20	20	18.55	2.53	1	0	0.11.0	87 P
U90919_at	9	0	20	20	18.45	1.86	0	0	0.1nf	86 P
X64838_at	13	0	20	20	18.65	3.25	0	0	0.1nf	86 P
Z69720_at	11	1	20	20	18.55	1.77	0	0	0.11.0	84 P
U82130_at	9	2	20	20	18.45	1.51	0	0	0.4.5	83 P
U90909_at	12	0	20	20	18.60	2.44	0	0	0.1nf	82 P
X78925_at	10	1	20	20	18.60	3.01	0	0	0.1nf	82 P
U90716_at	7	1	20	20	18.50	2.34	1	0	0.10.0	81 P
					18.35	1.53	0	0	0.7.0	

Connective tissue C											
X98261_at	9	2	20	20	18.045	1.18	0	0.45	81 P		
AFFX-M27830_5_at	7	0	20	20	18.035	1.44	0	0 Inf	80 P		
U90547_at	10	1	20	20	17.050	2.10	1	1 10.0	80 P		
X66364_at	8	1	20	20	18.040	0.91	0	0.80	80 P		
Z22548_at	8	1	20	20	17.040	1.97	0	0.80	80 P		
Z50853_at	11	2	20	20	18.055	1.81	0	0.55	80 P		
X78520_at	9	0	20	20	18.045	1.63	0	0 Inf	79 P		
U96113_at	11	1	20	20	18.055	3.13	1	0 11.0	78 P		
X68560_at	10	0	20	20	18.050	2.62	0	0 Inf	78 P		
Z37166_at	10	0	20	20	17.050	1.47	0	0 Inf	78 P		
U81006_at	10	0	20	20	18.050	3.41	1	0 Inf	76 P		
U81607_at	9	1	20	20	18.045	2.66	2	0.90	76 P		
X56807_at	10	0	20	20	18.050	3.00	0	0 Inf	76 P		
X68141_at	8	2	20	20	18.040	1.60	0	0.40	76 P		
X93921_at	11	1	20	20	18.055	2.22	0	0 11.0	76 P		
X87176_at	9	3	20	20	18.045	1.61	0	0.30	76 P		
Z23064_at	8	2	20	20	18.045	1.61	0	0.45	75 P		
X61100_ma1_at	10	2	20	20	18.050	2.21	0	0.50	74 P		
X63879_at	11	2	20	20	18.055	2.89	1	1.55	74 P		
Y12711_at	13	1	20	20	18.065	3.39	2	0 13.0	73 P		
Z72498_at	12	1	20	20	18.060	2.00	2	1 12.0	73 P		
X63973_at	10	2	20	20	17.050	2.51	1	0.50	72 P		
X64373_at	8	2	20	20	18.040	1.79	0	0.40	72 P		
Y08614_at	12	0	20	20	18.060	3.15	1	0 Inf	72 P		
Z29064_at	7	2	20	20	18.035	1.33	0	0.35	72 P		
U80017_ma3_at	11	1	20	20	18.055	2.56	0	0 11.0	71 P		
X72177_ma1_at	11	0	20	20	18.055	2.55	1	0 Inf	71 P		
X80230_at	11	3	20	20	18.055	1.45	0	0.37	71 P		
X63753_at	10	1	20	20	18.050	2.04	1	0 10.0	71 P		
X64330_at	10	1	20	20	18.050	2.63	1	0 10.0	70 P		
X81198_at	9	2	20	20	18.045	1.59	0	0.45	70 P		
X83378_at	7	1	20	20	18.035	2.33	1	0.70	70 P		
X98001_at	10	2	20	20	17.050	1.88	0	0.50	70 P		
U65928_at	8	1	20	20	18.040	1.30	0	0.80	70 P		
U70426_at	13	1	20	20	18.065	1.82	0	0 13.0	69 P		
X79353_at	8	2	20	20	18.040	1.24	0	0.40	69 P		
U76992_at	7	1	20	20	18.035	1.61	1	0.70	69 P		
U87408_at	9	2	20	20	18.045	1.85	1	0.45	68 P		
X07767_at	7	1	20	20	18.035	1.05	0	0.70	68 P		
X63563_at	7	2	20	20	17.035	1.41	0	0.35	68 P		
Y07867_at	10	2	20	20	18.050	2.81	1	0.50	68 P		
X77548_at	7	1	20	20	18.035	1.43	0	0.70	67 P		
Y11306_ma1_at	8	2	20	20	18.040	1.81	1	1.40	67 P		
Z22865_at	8	2	20	20	18.040	1.48	0	0.40	67 P		
AFFX-B10B-3_at	11	1	20	20	18.055	1.24	0	0 11.0	66 P		
X57522_at	11	3	20	20	18.055	2.04	0	0.37	65 P		
X91788_at	12	3	20	20	18.060	2.03	0	0.40	65 P		
U91327_at	8	2	20	20	17.040	2.45	1	0.40	64 P		
U77665_at	8	0	20	20	18.040	1.25	1	0 Inf	63 P		
X03635_at	11	2	20	20	18.055	1.87	0	0.55	63 P		
X58798_at	7	2	20	20	18.035	1.34	0	0.35	63 P		

Side 8

Connective tissue C																			
X72841_at	13	1	20	20	18 0.65	3.41	1	0	13.0	63 P									
X98325_at	8	1	20	20	18 0.40	1.08	0	0	0.80	63 P									
U76369_at	8	1	20	20	18 0.40	1.26	1	1	0.80	62 P									
X86397_at	11	0	20	20	17 0.55	2.33	0	0	0 Inf	62 P									
X59405_at	9	2	20	20	18 0.45	2.15	0	0	0.45	61 P									
Z68204_at	7	0	20	20	18 0.35	1.69	0	0	0 Inf	61 P									
U79297_at	11	1	20	20	18 0.55	3.42	2	2	0 11.0	60 P									
X16354_at	11	3	20	20	18 0.55	2.01	0	0	0.55	60 P									
X78627_at	11	3	20	20	18 0.55	2.48	0	0	0.37	60 P									
X55544_at	8	1	20	20	18 0.40	2.20	0	0	0.80	59 P									
Y09443_at	7	0	20	20	18 0.35	1.56	0	0	0 Inf	59 P									
U72508_at	7	1	20	20	18 0.35	1.24	0	0	0.70	58 P									
U73682_at	8	2	20	20	18 0.40	1.16	0	0	0.40	58 P									
U90549_at	8	2	20	20	18 0.40	1.45	0	0	0.40	58 P									
X53586_ma1_at	11	0	20	20	18 0.55	4.12	2	2	0 Inf	57 P									
-17227_at	10	2	20	20	18 0.50	1.95	1	1	0.50	57 P									
X67212_at	9	2	20	20	18 0.45	2.58	1	1	0.45	55 P									
K13482_at	7	1	20	20	18 0.35	1.10	0	0	0.70	54 P									
X63469_at	7	0	20	20	18 0.35	1.85	0	0	0 Inf	54 P									
U69141_at	7	1	20	20	18 0.35	1.20	0	0	0.70	53 P									
U71207_at	9	3	20	20	18 0.45	1.54	0	0	0.30	53 P									
U85992_at	9	2	20	20	18 0.45	1.82	0	0	0.45	52 P									
U79274_at	8	1	20	20	18 0.40	1.17	3	3	0.80	51 P									
U79281_at	13	0	20	20	17 0.65	4.11	0	0	0 Inf	50 P									
X63337_at	9	2	20	20	18 0.45	1.31	0	0	0.45	50 P									
X64229_at	10	3	20	20	18 0.50	1.38	1	1	0.33	50 P									
Z29331_at	11	2	20	20	18 0.55	3.98	3	3	0.55	50 P									
Z35491_at	8	0	20	20	17 0.40	2.75	1	1	0 Inf	50 P									
X16396_at	9	0	20	20	18 0.45	2.61	1	1	0 Inf	49 P									
X60673_ma1_at	9	2	20	20	18 0.45	1.80	0	0	0.45	49 P									
U66669_at	9	2	20	20	18 0.45	1.83	0	0	0.45	48 P									
U72342_at	10	3	20	20	18 0.50	1.41	0	0	0.33	48 P									
U83908_at	9	2	20	20	18 0.45	2.41	1	1	0.45	48 P									
X82396_at	8	2	20	20	18 0.40	2.11	1	1	0.40	48 P									
O86550_at	9	0	20	20	18 0.45	2.24	0	0	0 Inf	48 P									
X76648_at	9	1	20	20	18 0.46	2.11	0	0	0.90	47 P									
Z88129_cd51_at	7	1	20	20	18 0.35	1.03	0	0	0.70	47 P									
D10040_at	8	2	20	20	18 0.40	1.31	0	0	0.40	47 P									
U84573_at	9	1	20	20	18 0.45	3.00	2	2	0.90	46 P									
X54941_at	7	1	20	20	18 0.35	1.30	0	0	0.70	46 P									
X78057_at	8	2	20	20	18 0.40	1.11	1	1	0.40	46 P									
X98248_ma1_at	8	2	20	20	18 0.40	1.99	1	1	0.40	46 P									
Z24724_at	10	0	20	20	18 0.50	2.59	1	1	0 Inf	45 P									
U68111_at	8	0	20	20	18 0.45	1.75	0	0	0 Inf	45 P									
U94332_at	7	1	20	20	18 0.35	1.71	1	1	0.70	45 P									
X98172_at	8	0	20	20	18 0.45	1.23	0	0	0 Inf	45 P									
X62048_at	8	0	20	20	18 0.40	1.87	0	0	0 Inf	44 P									
X87241_at	10	2	20	20	18 0.50	2.53	0	0	0.50	44 P									
X94232_at	8	0	20	20	17 0.40	1.63	0	0	0 Inf	44 P									
Z95824_at	7	0	20	20	18 0.35	1.20	0	0	0 Inf	44 P									
X04011_at	10	2	20	20	18 0.50	1.47	0	0	0.50	43 P									
X98260_at	8	2	20	20	18 0.40	1.02	0	0	0.40	43 P									

Side 9

Connective tissue C									
X59841_at	8	0	20	20	18.040	1.55	0	0 Inf	42 P
X85644_at	7	1	20	20	17.035	0.97	0	0.70	42 P
X74262_at	9	2	20	20	18.045	2.21	0	0.45	42 P
X86586_at	8	1	20	20	18.045	1.20	0	0.80	42 P
U67319_at	7	1	20	20	18.035	0.93	1	0.70	41 P
X07024_at	8	1	20	20	18.040	1.31	0	0.80	41 P
X52520_at	9	1	20	20	18.045	2.59	0	0.90	41 P
U0912_at	8	1	20	20	18.040	1.12	0	0.80	40 P
X06946_at	8	2	20	20	18.040	1.65	1	0.40	40 P
X61118_mai_at	10	0	20	20	18.050	2.33	0	0 Inf	40 P
X81788_at	11	3	20	20	18.055	2.32	1	0.37	40 P
X53793_at	10	2	20	20	18.050	2.40	0	0.50	39 P
X54326_at	8	2	20	20	17.040	1.00	0	0.40	39 P
U86666_at	8	2	20	20	18.040	1.58	1	0.40	37 P
X73608_at	7	1	20	20	18.035	1.62	0	0.70	37 P
X84002_at	8	2	20	20	18.040	1.58	0	0.40	37 P
U69127_at	8	0	20	20	18.040	1.33	0	0 Inf	35 P
X17025_at	8	2	20	20	17.040	1.78	1	0.40	35 P
X57206_at	8	2	20	20	17.040	1.15	0	0.40	35 P
X76061_at	8	2	20	20	18.040	2.02	1	0.40	35 P
Z34897_at	8	1	20	20	18.040	1.45	0	0.80	35 P
Z37976_at	8	0	20	20	17.040	0.95	0	0 Inf	35 P
X57303_at	8	1	20	20	17.040	1.94	0	0.80	34 P
X83368_at	10	2	20	20	18.050	2.16	2	0.50	34 P
Y10313_at	8	2	20	20	18.040	1.25	0	0.40	34 P
X63417_at	7	1	20	20	18.035	1.43	0	0.70	33 P
X94910_at	8	1	20	20	18.040	1.26	0	0.80	32 P
U77718_at	9	2	20	20	18.045	1.27	0	0.45	31 P
U0916_at	10	2	20	20	18.050	3.47	3	0.50	31 P
X06562_at	9	2	20	20	18.045	2.44	1	0.45	31 P
U73960_at	9	2	20	20	17.045	1.15	0	0.45	30 P
X07820_at	8	1	20	20	17.040	1.86	1	0.80	30 P
X57025_at	7	0	20	20	17.035	1.51	0	0 Inf	30 P
D16481_at	8	1	20	20	18.040	1.23	0	0.80	29 P
U75679_at	8	1	20	20	18.040	1.51	0	0.80	29 P
X64195_at	7	2	20	20	18.035	2.65	2	0.35	28 P
Z46973_at	8	2	20	20	18.040	1.73	1	0.40	28 P
U79258_at	8	1	20	20	18.040	2.27	0	0.80	27 P
X58723_at	9	2	20	20	18.045	2.60	1	0.45	27 P
X92110_at	8	2	20	20	18.040	2.38	2	0.40	27 P
X99584_at	7	1	20	20	18.035	1.22	0	0.70	27 P
Z22535_at	8	2	20	20	17.040	1.20	0	0.40	27 P
U92015_at	8	2	20	20	18.040	1.13	0	0.40	26 P
X73882_at	8	2	20	20	18.040	1.58	0	0.40	26 P
U79245_at	8	2	20	20	17.040	2.65	2	0.40	25 P
X95592_at	10	2	20	20	17.050	1.79	0	0.50	25 P
U86561_at	7	2	20	20	18.035	1.32	0	0.35	23 P
U97018_at	9	3	20	20	18.045	1.38	1	0.30	22 P

Gene Name	Connective tissue D																Abn Cell
	Positiv		Nega		Palrs		Palrs		Pos		Fract		Log		Avg		
M26311_s_at	17	0	19	19	17	0.89	5.63	2	0	Inf					15733 P		
XG2426_s_at	19	0	20	20	18	0.95	4.86	0	0	Inf					13355 P		
M86757_s_at	20	0	20	20	18	1.00	6.88	2	0	Inf					10368 P		
L05187_at	20	0	20	20	18	1.00	5.41	1	0	Inf					6544 P		
hum_alu_at	62	0	69	69	65	0.90	4.64	2	0	Inf					5696 P		
L04483_s_at	18	0	17	17	15	0.94	6.22	3	0	Inf					5632 P		
L42601_f_at	19	0	20	20	18	0.95	5.80	2	0	Inf					5155 P		
L42563_f_at	20	0	20	20	18	1.00	6.01	3	0	Inf					4939 P		
J04617_s_at	17	0	18	18	16	0.94	5.76	1	0	Inf					4935 P		
V01516_f_at	19	0	20	20	18	0.85	8.01	2	0	Inf					4779 P		
M63438_s_at	15	0	17	17	15	0.88	5.15	0	0	Inf					4579 P		
L05188_f_at	19	0	20	20	18	0.95	6.42	2	0	Inf					4465 P		
M19888_at	19	0	20	20	18	0.95	6.24	3	0	Inf					4441 P		
X53065_f_at	20	0	20	20	18	1.00	5.72	1	0	Inf					4285 P		
AFFX-HSAC07/X00351_M_at	20	0	20	20	18	1.00	5.33	0	0	Inf					4239 P		
X03689_s_at	18	0	18	18	17	1.00	7.09	1	0	Inf					4233 P		
X00351_f_at	19	0	20	20	18	0.95	7.19	2	0	Inf					4186 P		
AFFX-HUNGAPDH/M33197_3_at	19	0	20	20	18	0.95	5.92	1	0	Inf					4106 P		
X09482_f_at	2	0	3	3	3	0.67	2.08	0	0	Inf					3885 P		
M20030_f_at	20	0	20	20	18	1.00	6.64	4	0	Inf					3809 P		
M10277_s_at	19	0	20	20	18	0.95	5.59	3	0	Inf					3788 P		
J00105_s_at	20	0	20	20	18	1.00	8.04	5	0	Inf					3684 P		
X76223_s_at	18	1	20	20	18	0.90	4.92	1	1	18.0					3490 P		
M87769_s_at	18	1	20	20	18	0.90	4.97	1	0	18.0					3447 P		
HC2815-HT4023_s_at	19	0	20	20	18	0.95	5.41	1	0	Inf					3415 P		
01677_f_at	19	0	20	20	18	0.95	5.08	1	0	Inf					3234 P		
FFX-Crux-3_at	19	0	20	20	18	1.00	6.09	1	0	Inf					3222 P		
157348_s_at	19	0	20	20	18	0.95	6.81	2	0	Inf					3203 P		
AFFX-HSAC07/X00351_3_at	15	0	19	19	17	0.79	4.47	1	0	Inf					3031 P		
D49824_s_at	17	0	20	20	18	0.85	5.00	0	0	Inf					2862 P		
U43901_ma1_e_at	7	0	7	7	7	1.00	5.51	0	0	Inf					2821 P		
V00594_s_at	18	0	20	20	18	0.90	5.08	0	0	Inf					2812 P		
AFFX-HSAC07/X00351_5_at	11	0	12	12	10	0.92	6.41	1	0	Inf					2805 P		
D13413_ma1_s_at	18	0	20	20	18	0.90	5.13	0	0	Inf					2776 P		
U08155_s_at	17	0	18	18	16	0.94	5.38	0	0	Inf					2651 P		
AFFX-Crux-5_at	12	1	14	14	12	0.86	5.03	0	1	12.0					2575 P		
AFFX-HUNGAPDH/M33197_M_at	19	0	20	20	18	0.95	7.15	2	0	Inf					2535 P		
S82287_at	16	1	20	20	18	0.90	4.41	0	0	16.0					2457 P		
Z49148_s_at	19	0	20	20	18	0.95	4.22	0	0	Inf					2360 P		
HG2815-HT2931_at	20	0	20	20	18	1.00	5.62	1	0	Inf					2303 P		
M31520_ma1_s_at	5	0	6	6	6	0.83	4.17	0	0	Inf					2265 P		
M34516_at	15	0	16	16	14	0.94	6.19	2	0	Inf					2242 P		
M36072_at	5	0	5	5	5	1.00	4.11	0	0	Inf					2235 P		
AFFX-HUNGAPDH/M33197_5_at	16	0	20	20	18	0.80	4.10	0	0	Inf					2150 P		
M56409_s_at	18	0	20	20	18	0.90	5.78	3	0	Inf					2104 P		
L42611_f_at	14	0	20	20	18	0.70	3.86	0	0	Inf					1946 P		
X57351_s_at	12	0	12	12	10	1.00	5.81	0	0	Inf					1945 P		
HG2815-HT2931_s_at	13	0	14	14	12	0.93	6.37	0	0	Inf					1926 P		
X53296_s_at	19	0	20	20	18	0.85	5.49	3	0	Inf					1652 P		
M55898_s_at	18	0	20	20	18	0.80	6.05	2	0	Inf					1610 P		
X04470_s_at	18	0	19	19	17	0.95	5.06	1	0	Inf					1525 P		

Slide 1

Connective tissue D										
M24485_s_at	17	0	20	20	18.85	3.86	0	0	Inf	1522 P
S71043_mai1_s_at	16	0	20	20	18.80	3.68	1	0	Inf	1473 P
X51345_at	16	1	20	20	18.80	5.18	3	0	16.0	1446 P
HG4068-HT4339_s_at	18	0	20	20	18.90	5.56	2	0	Inf	1416 P
Y07909_at	16	1	20	20	18.80	6.79	5	1	16.0	1399 P
J04152_mai1_s_at	18	0	20	20	18.90	5.26	1	0	Inf	1311 P
Z48501_s_at	16	1	19	19	17.84	5.15	0	0	16.0	1263 P
S68896_at	17	1	20	20	18.85	5.37	0	0	17.0	1239 P
AFFX-BioDn-3_at	14	2	20	20	18.70	3.13	0	0	7.0	1215 P
X56681_s_at	15	2	20	20	18.75	4.09	1	0	7.5	1204 P
U19557_s_at	20	0	20	20	18.100	5.25	0	0	Inf	1195 P
Z19564_g_at	16	1	18	18	16.89	5.89	1	1	16.0	1186 P
S54005_s_at	19	0	20	20	18.95	5.92	1	0	Inf	1175 P
U68105_s_at	15	0	20	20	18.75	6.45	6	0	Inf	1173 P
HG417-HT417_s_at	18	0	20	20	18.85	5.40	2	0	Inf	1172 P
HG3431-HT3616_s_at	18	0	20	20	18.90	5.80	1	0	Inf	1126 P
M64860_f_at	30	0	40	40	39.75	3.63	0	0	Inf	1095 P
S72493_s_at	17	1	20	20	18.85	2.94	0	0	17.0	1072 P
U20734_s_at	16	0	20	20	18.80	3.73	1	0	Inf	1069 P
M34516_f_at	11	0	11	11	9.100	5.23	1	0	Inf	1058 P
X69554_at	17	0	20	20	18.85	4.74	0	0	Inf	1050 P
M92843_s_at	19	0	20	20	18.95	5.73	0	0	Inf	1028 P
M13560_s_at	15	0	20	20	18.75	3.95	1	0	Inf	952 P
U57341_f_at	1	0	2	2	2.050	2.92	0	0	Inf	941 P
L33930_s_at	15	1	20	20	18.75	4.28	0	0	15.0	917 P
M26709_s_at	19	0	20	20	18.95	5.11	3	0	Inf	917 P
X04347_s_at	18	0	20	20	18.90	4.90	1	0	Inf	911 P
HG1980-HT2023_at	12	0	20	20	18.60	2.78	0	0	Inf	903 P
HG658-HT658_f_at	30	0	40	40	39.75	3.12	0	0	Inf	889 P
M11313_s_at	17	1	20	20	18.85	5.16	2	0	17.0	842 P
M83667_mai1_g_at	17	0	20	20	18.85	3.60	0	0	Inf	838 P
M19311_s_at	12	1	16	16	14.075	5.56	0	0	12.0	822 P
M14328_s_at	14	1	20	20	18.70	3.92	0	0	14.0	819 P
X57351_at	5	0	8	8	8.63	2.90	0	0	Inf	816 P
L06643_s_at	13	0	19	19	17.68	2.94	0	0	Inf	802 P
N21142_cds2_g_at	13	2	20	20	18.65	3.48	0	0	6.5	782 P
Z68228_s_at	15	1	20	20	18.75	3.28	0	0	15.0	779 P
HG2797-HT2906_s_at	15	0	19	19	17.79	3.82	0	0	Inf	759 P
D32129_f_at	17	0	20	20	18.85	4.75	0	0	Inf	753 P
X57809_s_at	9	1	12	12	10.75	2.45	0	0	9.0	737 P
V00594_at	3	1	8	8	8.38	2.72	0	0	3.0	715 P
HG1515-HT1515_f_at	16	0	20	20	18.80	5.27	2	0	Inf	662 P
HG3342-HT3519_s_at	16	0	19	19	17.84	4.66	0	0	Inf	660 P
S75256_s_at	17	1	20	20	18.85	4.50	3	0	17.0	655 P
M18045_f_at	14	1	20	20	18.70	4.81	4	0	14.0	644 P
M14463_mai1_s_at	13	0	20	20	18.65	3.12	0	0	Inf	641 P
Z30643_at	10	3	20	20	17.90	2.07	0	0	3.3	640 P
AFFX-HSAC07X00351_3_at	15	0	20	20	18.75	3.82	0	0	Inf	629 P
X95240_s_at	13	2	20	20	18.65	3.73	4	1	6.5	626 P
M33600_f_at	16	0	20	20	18.60	3.73	0	0	Inf	619 P
X14008_mai1_f_at	13	2	20	20	18.65	4.15	3	0	6.5	602 P
M21302_at	14	1	20	20	18.70	4.11	2	0	14.0	600 P
X12671_mai1_at	20	0	20	20	18.100	4.55	0	0	Inf	594 P
L12711_s_at	11	1	19	19	17.058	3.30	1	0	11.0	589 P

Slide 2

Side 2

Connective tissue D																			
M12125_at	12	2	20	20	18 0.60	2.30	0	0.0	586 P										
M58076_at	10	1	20	20	18 0.50	2.18	0	0 10.0	573 P										
J03801_f_at	13	1	20	20	18 0.65	5.62	3	0 13.0	557 P										
D86974_at	15	2	20	20	18 0.75	2.56	0	0 7.5	519 P										
J03077_s_at	11	1	20	20	18 0.55	3.21	0	0 11.0	510 P										
M54915_s_at	13	0	20	20	18 0.65	3.37	0	0 Inf	500 P										
HG3236-HT3413_f_at	12	1	20	20	18 0.60	3.01	0	0 12.0	490 P										
D17408_s_at	14	0	20	20	18 0.70	3.72	0	0 Inf	483 P										
M26730_s_at	17	1	20	20	18 0.85	5.65	2	0 17.0	465 P										
X05130_s_at	12	2	19	19	17 0.63	2.54	0	1 6.0	464 P										
U14394_at	11	3	20	20	18 0.55	2.95	0	0 3.7	456 P										
X17093_at	12	1	20	20	18 0.60	2.73	1	0 12.0	435 P										
L33075_at	17	0	20	20	18 0.85	4.20	1	0 Inf	432 P										
HG3597-HT3800_f_at	15	1	20	20	17 0.75	4.30	2	0 15.0	422 P										
U43916_s_at	15	0	20	20	18 0.75	3.48	0	0 Inf	408 P										
L40397_at	12	1	20	20	18 0.60	2.35	0	0 12.0	407 P										
HG1428-HT1428_s_at	15	0	20	20	18 0.75	4.25	1	0 Inf	401 P										
X02761_s_at	14	0	20	20	18 0.70	3.69	0	0 Inf	397 P										
X12876_s_at	15	1	20	20	18 0.75	4.25	0	0 15.0	385 P										
X99133_at	9	2	20	20	18 0.45	1.79	0	0 4.5	384 P										
L11672_at	6	0	12	12	10 0.50	2.17	0	0 Inf	370 P										
HG2917-HT3051_f_at	12	0	20	20	18 0.60	2.29	0	0 Inf	370 P										
HG3576-HT3779_f_at	11	2	20	20	18 0.55	2.86	0	0 5.5	365 P										
U00947_s_at	19	0	20	20	18 0.95	5.49	3	0 Inf	361 P										
HG2916-HT3059_f_at	10	0	20	20	17 0.50	2.22	0	0 Inf	351 P										
Z48835_s_at	14	3	20	20	18 0.70	3.25	1	1 4.7	349 P										
HG2994-HT4850_s_at	8	2	20	20	18 0.40	1.29	0	0 4.0	348 P										
D43682_s_at	9	3	20	20	18 0.45	2.40	0	0 3.0	345 P										
Z69043_s_at	14	2	20	20	18 0.70	2.39	0	0 7.0	344 P										
AFFX-BloDn-5_at	16	1	20	20	18 0.80	3.44	0	0 16.0	342 P										
X95325_s_at	11	3	20	20	18 0.55	1.91	0	0 3.7	340 P										
HG1322-HT5143_s_at	14	1	20	20	18 0.70	4.19	0	0 14.0	339 P										
AFFX-BloC-5_at	16	1	20	20	18 0.80	3.17	0	0 16.0	337 P										
J02683_s_at	11	0	20	20	18 0.55	2.60	0	0 Inf	337 P										
M62403_s_at	12	1	20	20	18 0.60	3.02	1	0 12.0	327 P										
U48705_maf1_s_at	12	1	20	20	18 0.60	3.10	1	0 12.0	313 P										
M33493_s_at	14	4	20	20	18 0.70	2.77	0	0 3.5	311 P										
U92314_s_at	16	2	20	20	18 0.80	4.10	1	0 8.0	305 P										
X15729_s_at	14	0	20	20	18 0.70	3.11	0	0 Inf	297 P										
U05861_at	9	2	20	20	18 0.45	1.93	0	0 4.5	296 P										
X13461_s_at	12	1	20	20	18 0.60	2.88	0	0 12.0	288 P										
U70439_s_at	9	1	19	19	17 0.47	2.77	2	0 9.0	284 P										
M19267_s_at	13	1	20	20	18 0.65	2.85	0	0 13.0	279 P										
L09209_s_at	13	2	20	20	18 0.65	2.04	0	0 6.5	278 P										
V00569_s_at	13	0	20	20	18 0.85	3.30	0	0 Inf	277 P										
M16750_s_at	7	0	20	20	18 0.35	1.76	0	0 Inf	270 P										
M54046_at	14	1	20	20	18 0.70	3.97	1	1 14.0	251 P										
M65292_s_at	9	0	15	15	17 0.47	3.02	0	0 Inf	246 P										
M12953_s_at	10	0	20	20	17 0.50	2.40	1	0 Inf	246 P										
M13690_s_at	14	1	20	20	18 0.70	2.43	0	0 14.0	244 P										
U72649_at	17	0	20	20	18 0.85	4.88	1	0 Inf	241 P										
M28213_s_at	14	0	20	20	17 0.70	3.31	1	0 Inf	239 P										
HG3076-HT3238_s_at	12	2	20	20	17 0.60	2.84	0	0 6.0	239 P										
M30448_s_at																			

Side 3

Connective tissue D

M34896_s_at	17	0	20	20	18 0.85	4.33	1	0 Inf	232 P
D17793_at	14	2	20	20	18 0.70	2.78	0	0 7.0	232 P
X52022_at	13	1	20	20	17 0.65	2.97	0	0 13.0	231 P
X06700_s_at	16	0	20	20	18 0.80	4.50	2	0 Inf	229 P
Y00787_s_at	12	0	20	20	18 0.60	2.65	0	0 Inf	224 P
U16799_s_at	14	2	20	20	18 0.70	3.85	2	0 7.0	223 P
X57152_rna1_s_at	14	2	20	20	18 0.70	2.80	0	0 7.0	223 P
D87017_cd63_at	8	0	20	20	18 0.40	1.43	0	0 Inf	222 P
U05681_s_at	12	2	20	20	18 0.60	1.94	0	0 6.0	221 P
M31551_s_at	13	1	20	20	18 0.65	3.30	1	1 13.0	219 P
X01703_at	14	2	20	20	18 0.70	2.83	1	0 7.0	218 P
J02621_s_at	11	0	20	20	18 0.55	2.51	1	0 Inf	217 P
M21538_at	13	0	20	20	18 0.65	2.60	1	0 Inf	215 P
L13740_at	7	0	20	20	18 0.35	1.21	0	0 Inf	212 P
X52979_rna1_s_at	14	1	20	20	18 0.70	2.51	0	0 14.0	209 P
M27438_s_at	13	0	20	20	18 0.65	3.39	0	0 Inf	206 P
J03805_s_at	16	0	18	18	16 0.89	5.53	3	0 Inf	206 P
X17587_s_at	10	2	20	20	17 0.50	2.32	0	0 5.0	206 P
M32304_s_at	9	2	20	20	18 0.45	1.56	0	0 4.5	202 P
M16342_at	13	1	20	20	17 0.65	2.88	0	0 13.0	201 P
M16652_at	3	0	4	4	4 0.75	2.05	0	0 Inf	201 P
X03066_f_at	18	3	40	40	38 0.45	1.61	0	0 6.0	194 P
M23323_s_at	11	2	20	20	18 0.55	1.80	0	0 5.5	192 P
K02405_f_at	10	2	20	20	18 0.50	1.27	0	0 5.0	192 P
HG4535-HT4940_s_at	8	1	20	20	18 0.40	1.14	0	0 8.0	191 P
M57466_s_at	9	2	20	20	18 0.45	2.18	0	0 4.5	188 P
M97935_s_at	13	2	20	20	18 0.65	2.71	0	0 6.5	186 P
X04528_at	14	1	20	20	18 0.70	2.32	0	0 14.0	185 P
U29874_s_at	13	2	20	20	18 0.65	2.72	0	0 6.5	185 P
U04636_rna1_at	11	1	20	20	18 0.55	1.99	0	1 11.0	184 P
Z15115_at	14	2	20	20	18 0.70	2.33	0	0 7.0	184 P
X72727_at	15	1	20	20	18 0.75	3.16	0	0 15.0	183 P
Y00264_at	13	1	20	20	17 0.65	3.58	0	0 13.0	183 P
AFFX-BioC-3_at	11	0	20	20	18 0.55	1.90	0	0 Inf	175 P
HG3044-HT3742_s_at	11	0	20	20	18 0.55	2.78	0	0 Inf	175 P
U61734_s_at	10	1	19	19	17 0.53	2.84	1	0 10.0	175 P
L49380_at	8	2	20	20	18 0.40	1.18	0	0 4.0	171 P
D10867_s_at	14	1	17	17	15 0.82	3.23	0	0 14.0	170 P
D78577_s_at	11	1	20	20	18 0.55	2.47	2	0 11.0	170 P
D83174_s_at	9	0	20	20	17 0.45	1.86	0	0 Inf	169 P
M37457_at	3	0	4	4	4 0.75	2.10	0	0 Inf	168 P
D78132_s_at	14	0	20	20	18 0.70	5.12	2	0 Inf	167 P
X71345_f_at	9	2	20	20	18 0.45	1.93	1	0 4.5	166 P
U08021_at	10	0	20	20	17 0.50	2.15	0	0 Inf	165 P
U01691_s_at	9	0	20	20	18 0.45	3.00	3	0 Inf	164 P
M83216_s_at	15	1	20	20	18 0.75	3.89	0	0 15.0	163 P
HG688-HT688_f_at	10	1	20	20	18 0.50	1.61	0	0 10.0	163 P
M30703_s_at	10	1	20	20	18 0.50	2.67	1	1 10.0	160 P
U79528_s_at	7	0	20	20	18 0.35	1.46	0	0 Inf	160 P
M83651_at	10	0	20	20	18 0.50	2.68	1	0 Inf	159 P
HG4641-H14946_s_at	10	0	18	18	16 0.56	2.35	0	0 Inf	159 P
X73358_s_at	9	1	19	19	17 0.47	1.75	1	0 9.0	159 P
Z35402_rna1_s_at	10	1	20	20	18 0.50	2.27	0	0 10.0	159 P
U12767_at	13	0	20	20	17 0.65	2.37	0	0 Inf	154 P

Side 4

68

Connective tissue D

U36341_rna1_at	7	1	20	20	18.035	1.08	0	0.7.0	98 P
U22431_s_at	12	1	20	20	17.060	2.37	0	0.12.0	88 P
M60874_s_at	7	0	20	20	17.035	1.28	0	0.1nf	98 P
AFFX-BioB-5_at	8	2	20	20	18.040	1.15	0	0.4.0	85 P
D42040_s_at	8	2	20	20	18.040	1.51	0	0.4.0	94 P
U67122_s_at	11	1	20	20	18.055	2.43	0	0.11.0	94 P
U28014_at	13	0	20	20	18.065	3.23	1	0.1nf	94 P
D78206_s_at	8	0	20	20	17.040	1.32	0	0.1nf	93 P
S78771_s_at	10	3	20	20	18.050	1.91	0	0.3.3	92 P
M58525_s_at	7	1	20	20	18.035	1.20	0	0.7.0	92 P
M60483_rna1_s_at	9	1	18	18	16.050	2.65	1	0.9.0	92 P
HG2868-HT3012_s_at	9	2	20	20	18.045	2.18	1	0.4.5	91 P
U41518_at	10	0	20	20	18.050	1.67	0	0.1nf	90 P
Z74615_at	8	1	20	20	17.040	1.76	1	0.8.0	90 P
Z35085_s_at	14	1	18	18	17.074	4.26	1	0.14.0	80 P
L76517_at	7	0	20	20	17.035	1.61	0	0.1nf	89 P
M16276_at	9	1	20	20	18.045	1.76	0	0.9.0	89 P
D45917_s_at	10	2	20	20	18.050	2.13	2	1.5.0	88 P
U19495_s_at	15	1	20	20	17.075	4.92	4	0.15.0	88 P
X07438_s_at	14	2	19	19	17.074	3.49	1	0.7.0	88 P
U41740_at	12	2	20	20	18.060	2.58	1	0.6.0	86 P
X03363_s_at	9	1	20	20	18.045	1.54	0	0.9.0	86 P
M28882_s_at	8	1	17	17	15.047	2.28	1	0.8.0	85 P
HG4322-HT4582_at	11	2	20	20	18.055	2.59	1	0.5.5	85 P
L38490_s_at	7	1	20	20	18.035	1.30	0	0.7.0	84 P
X62083_s_at	7	1	20	20	18.035	1.31	1	0.7.0	84 P
U43944_at	12	1	20	20	18.060	2.44	0	0.12.0	84 P
HG3364-HT3876_s_at	9	0	20	20	18.045	2.10	0	0.1nf	83 P
X62534_s_at	10	0	20	20	18.050	2.63	0	0.1nf	83 P
Y00097_s_at	8	2	20	20	18.040	1.73	0	0.4.0	82 P
S72024_s_at	8	1	20	20	18.040	1.57	0	0.8.0	82 P
U72509_s_at	10	1	19	19	16.053	2.19	0	0.10.0	82 P
X65488_at	12	0	20	20	18.060	2.37	1	0.1nf	81 P
L32831_s_at	11	2	20	20	18.055	1.13	0	0.5.5	81 P
U45448_s_at	10	3	20	20	18.050	1.88	0	0.3.3	81 P
M20867_s_at	9	1	17	17	14.053	1.70	0	0.9.0	78 P
U30827_s_at	13	1	20	20	17.065	3.56	2	0.13.0	78 P
M31832_at	8	2	20	20	18.040	1.12	0	0.4.0	79 P
Z69030_s_at	6	1	18	18	16.033	1.85	1	0.6.0	78 P
HG3638-HT3849_s_at	9	1	20	20	18.045	1.88	1	0.8.0	77 P
U35005_s_at	10	2	20	20	18.050	2.08	0	0.5.0	76 P
HG2981-HT3127_s_at	11	1	19	19	17.058	1.75	0	0.11.0	75 P
D14826_s_at	7	1	20	20	18.035	1.19	0	0.7.0	74 P
M63838_s_at	8	0	20	20	18.045	2.69	1	0.1nf	73 P
Y00451_s_at	8	0	20	20	18.040	1.34	0	0.1nf	73 P
U19247_rna1_s_at	10	2	20	20	18.050	2.37	0	0.5.0	72 P
J04093_s_at	10	0	20	20	18.050	1.92	0	0.1nf	72 P
X60003_s_at	8	2	20	20	18.045	1.58	0	0.4.5	72 P
M61832_s_at	8	2	20	20	18.040	1.11	0	0.4.0	71 P
U01337_at	7	1	20	20	18.035	1.14	0	0.7.0	68 P
Z28491_s_at	10	0	20	20	18.050	2.52	1	0.1nf	66 P
U33936_s_at	12	2	20	20	18.060	1.80	0	0.6.0	66 P
S68805_at	10	0	20	20	18.050	2.36	0	0.1nf	65 P
D83260_s_at	8	1	19	19	16.042	1.83	0	0.8.0	65 P

Slide 6

Connective tissue D																			
U20938_at	11	0	20	20	20	18	0.55	1.93	0	0	Inf	64 P							
HG1400-HT1400_s_at	11	2	20	20	20	18	0.55	2.42	0	0	5.5	63 P							
L14778_s_at	12	0	19	19	17	0.63	4.34	4.34	4	0	Inf	61 P							
U96131_at	8	1	20	20	18	0.40	1.46	1.46	1	0	8.0	60 P							
M17183_s_at	8	1	20	20	18	0.40	1.95	1.95	1	0	8.0	60 P							
L00634_s_at	10	1	19	19	17	0.53	3.14	3.14	2	0	10.0	60 P							
U56046_s_at	12	1	20	20	18	0.60	3.04	3.04	1	0	12.0	58 P							
X53002_s_at	8	2	20	20	18	0.40	1.14	1.14	0	0	4.0	59 P							
X69820_s_at	8	1	20	20	18	0.40	2.17	2.17	0	0	8.0	59 P							
U33062_s_at	8	0	20	20	17	0.40	3.36	3.36	1	0	Inf	59 P							
U44103_at	10	2	20	20	17	0.50	2.57	2.57	0	0	5.0	59 P							
D28473_s_at	10	2	20	20	18	0.50	2.16	2.16	0	0	5.0	58 P							
U60061_at	9	2	20	20	18	0.45	2.22	2.22	2	0	4.5	57 P							
M21119_s_at	7	1	20	20	18	0.35	0.54	0.54	0	0	7.0	57 P							
U33838_at	2	0	4	4	4	0.50	2.70	2.70	0	0	Inf	57 P							
M24736_s_at	7	1	20	20	18	0.35	1.12	1.12	0	0	7.0	57 P							
HG4518-HT4921_c_at	1	0	2	2	2	0.50	1.26	1.26	0	0	Inf	56 P							
HG4557-HT4962_c_at	3	0	5	5	5	0.60	1.98	1.98	0	0	Inf	56 P							
S77410_at	7	1	20	20	18	0.35	1.04	1.04	0	0	7.0	55 P							
HG2090-HT2152_s_at	7	2	19	19	17	0.37	1.63	1.63	1	1	3.5	55 P							
X81625_at	9	1	20	20	18	0.45	2.01	2.01	1	0	9.0	54 P							
U41766_s_at	8	2	20	20	18	0.40	1.27	1.27	1	0	4.0	53 P							
U61276_s_at	9	2	20	20	18	0.45	2.01	2.01	0	0	4.5	53 P							
Y07566_at	9	1	20	20	18	0.45	1.50	1.50	0	0	9.0	53 P							
U33632_at	12	1	20	20	17	0.60	3.09	3.09	1	0	12.0	52 P							
M10321_s_at	7	1	20	20	18	0.35	1.12	1.12	0	0	7.0	52 P							
J03834_s_at	9	2	20	20	18	0.45	1.91	1.91	0	0	4.5	51 P							
X14253_s_at	8	2	20	20	18	0.40	1.76	1.76	0	0	4.0	51 P							
L15326_s_at	10	1	20	20	18	0.50	1.91	1.91	0	0	10.0	50 P							
M75715_s_at	9	1	19	19	17	0.47	2.08	2.08	0	0	8.0	50 P							
L08010_at	8	2	20	20	17	0.40	1.72	1.72	0	0	4.0	50 P							
M31516_s_at	7	0	20	20	18	0.35	1.37	1.37	0	0	Inf	49 P							
M96843_at	8	2	20	20	18	0.40	0.99	0.99	0	0	4.0	48 P							
X75918_at	11	2	20	20	18	0.55	1.77	1.77	0	0	5.5	48 P							
D28235_s_at	10	1	20	20	18	0.50	1.49	1.49	0	0	10.0	47 P							
M18508_xp13_s_at	8	1	20	20	18	0.40	0.95	0.95	0	0	8.0	47 P							
S79219_s_at	9	3	20	20	18	0.45	1.79	1.79	0	0	3.0	46 P							
L35249_s_at	7	1	18	18	16	0.39	1.78	1.78	0	0	7.0	45 P							
U84388_at	10	0	20	20	18	0.50	3.54	3.54	1	0	Inf	45 P							
AFFX-HUMTFR/M11507_s_at	9	2	20	20	18	0.45	1.08	1.08	0	0	4.5	44 P							
HG2743-HT3926_s_at	12	1	20	20	18	0.60	1.82	1.82	0	0	12.0	44 P							
HG545-HT345_s_at	9	2	20	20	18	0.45	1.08	1.08	0	0	4.5	44 P							
U69140_s_at	7	1	18	18	16	0.39	2.73	2.73	1	0	7.0	44 P							
AFFX-HUMRGE/M10098_M1_at	7	1	20	20	18	0.35	1.75	1.75	0	0	7.0	42 P							
U73936_at	8	2	20	20	18	0.40	1.14	1.14	0	0	4.0	42 P							
AB000381_s_at	9	2	20	20	18	0.45	2.66	2.66	2	0	4.5	42 P							
M28610_at	9	2	14	14	12	0.64	4.77	4.77	4	0	4.5	42 P							
U04265_s_at	9	3	20	20	17	0.35	1.90	1.90	1	0	3.0	42 P							
HG3075-HT3236_s_at	7	2	20	20	17	0.35	1.57	1.57	2	0	3.5	40 P							
X54993_s_at	8	2	20	20	18	0.40	1.29	1.29	1	0	4.0	40 P							
U61397_s_at	7	1	20	20	18	0.35	1.56	1.56	0	0	7.0	40 P							
X69886_s_at	7	0	19	19	17	0.37	1.26	1.26	0	0	Inf	40 P							
S82587_ma1_s_at	9	1	20	20	18	0.45	1.21	1.21	0	0	9.0	39 P							
X06182_s_at	8	1	20	20	18	0.40	1.48	1.48	1	0	8.0	38 P							

Side 7

Normal urothelium A

Pos/Neg Pair Pos Fr Log Av P/M 1 MM Pos/N Avg Diff Abs Call

Gene Name

hum_ali_at	69	0	69	69	67	1.00	7.38	12	0	Inf	27021 P
.06499_at	20	0	20	20	18	1.00	7.57	3	0	Inf	12530 P
R33214-HT3391_at	19	0	20	20	18	0.95	7.36	4	0	Inf	8561 P
AFFX-CreX-3_at	19	0	20	20	18	0.95	8.08	2	0	Inf	5861 P
HG3384-HT3541_at	20	0	20	20	18	1.00	7.78	7	0	Inf	5937 P
M13934_cds2_at	19	0	20	20	18	0.95	5.91	1	0	Inf	5721 P
HG1800-HT1823_at	19	0	20	20	18	0.95	7.68	4	0	Inf	5403 P
M17888_at	18	0	20	20	18	0.90	5.81	1	0	Inf	5130 P
M11147_at	18	0	20	20	18	0.90	6.85	3	0	Inf	4610 P
D45370_at	19	0	20	20	18	0.95	5.40	2	0	Inf	4549 P
HG2873-HT3017_at	18	0	20	20	18	0.90	7.15	3	0	Inf	4508 P
AFFX-CreX-5_at	20	0	20	20	18	1.00	7.29	4	0	Inf	4443 P
M18000_at	20	0	20	20	18	1.00	8.01	6	0	Inf	4368 P
D23660_at	19	0	20	20	18	0.95	7.99	6	0	Inf	4257 P
L08505_at	17	0	20	20	18	0.85	5.35	2	0	Inf	4184 P
HG3548-HT3751_at	19	0	20	20	18	0.95	6.73	3	0	Inf	4127 P
M17885_at	19	1	20	20	18	0.95	6.97	2	0	19.0	3868 P
AFFX-HUMIGAPDH/M331	19	0	20	20	18	0.95	5.62	1	0	Inf	3862 P
L38941_at	20	0	20	20	18	1.00	8.04	5	0	Inf	3734 P
AFFX-BioDn-3_at	17	0	20	20	18	0.85	4.18	0	0	Inf	3458 P
HG2789-HT2896_at	18	0	20	20	18	0.90	6.08	1	0	Inf	3126 P
M17733_at	18	0	20	20	18	0.90	6.92	3	0	Inf	2882 P
D79205_at	20	0	20	20	18	1.00	8.85	8	0	Inf	2864 P
L19527_at	18	0	20	20	18	0.90	5.82	2	0	Inf	2522 P
D78361_at	18	0	20	20	18	0.90	5.73	0	0	Inf	2513 P
AFFX-HSAC07/X00351_3	18	0	20	20	18	0.90	5.45	1	0	Inf	2382 P
D14530_at	20	0	20	20	18	1.00	7.43	3	0	Inf	2301 P
HG821-HT821_at	18	0	20	20	18	0.90	5.85	2	0	Inf	1918 P
HG813-HT813_at	18	0	20	20	17	0.95	6.85	5	0	Inf	1834 P
HG4319-HT4588_at	19	0	20	20	18	0.95	6.06	1	0	Inf	1746 P
HG384-HT384_at	12	0	20	20	17	0.60	4.27	2	0	Inf	1634 P
L20941_at	15	0	20	20	17	0.75	3.62	1	0	Inf	1530 P
HG4542-HT4847_at	17	0	20	20	18	0.85	5.16	1	0	Inf	1500 P
HG311-HT311_at	18	1	20	20	17	0.90	6.14	3	0	18.0	1484 P
AC002115_cds1_at	16	0	20	20	18	0.80	4.81	0	0	Inf	1456 P
AC002115_cds4_at	16	0	20	20	18	0.80	3.23	0	0	Inf	1382 P
M11353_at	16	1	20	20	17	0.80	6.14	3	0	16.0	1359 P
HG33-HT33_at	18	0	20	20	17	0.90	5.44	1	0	Inf	1327 P
D00017_at	16	0	20	20	18	0.80	4.46	0	0	Inf	1293 P
L11568_at	14	0	20	20	18	0.70	3.86	0	0	Inf	1195 P
D87735_at	17	0	20	20	17	0.85	4.52	1	0	Inf	1192 P
AFFX-HSAC07/X00351_A	18	1	20	20	18	0.90	3.90	0	0	18.0	1181 P
J04164_at	11	2	20	20	18	0.55	2.83	2	0	5.5	1186 P
J03592_at	17	1	20	20	18	0.85	4.77	1	0	17.0	1140 P
HG862-HT682_at	9	2	20	20	18	0.45	2.67	0	0	4.5	955 P
L19686_ma1_at	14	2	20	20	18	0.70	3.02	0	0	7.0	919 P
L26247_at	15	0	20	20	18	0.75	4.10	0	0	Inf	888 P

Side 1

Normal urothelium A

HG2279-HT2375_at	16	0	20	20	18	0.80	2.80	1	0	Inf	872 P
D86667_at	17	1	20	20	18	0.85	5.25	0	0	Inf	842 P
D36583_at	18	1	20	20	18	0.90	4.35	1	0	18.0	841 P
AFFX-HSAC07X00351_5	16	1	20	20	18	0.80	4.03	1	0	16.0	829 P
D00654_at	15	0	20	20	18	0.75	3.92	1	0	Inf	751 P
D30655_at	14	0	20	20	18	0.70	4.02	1	0	Inf	728 P
AFFX-HUMGAPDH/M331	14	2	20	20	18	0.70	2.59	0	0	7.0	725 P
M18283_at	15	2	20	20	18	0.75	3.61	1	0	7.5	725 P
M18961_at	14	3	20	20	18	0.70	2.67	2	0	4.7	705 P
J03827_at	13	0	20	20	18	0.65	3.12	0	0	Inf	694 P
AFFX-BioDn-5_at	11	0	20	20	18	0.55	2.70	0	0	Inf	692 P
D63874_at	12	1	20	20	18	0.60	3.74	3	0	12.0	675 P
J03181_at	17	0	20	20	18	0.85	4.97	0	0	Inf	668 P
J04823_msa1_at	15	1	20	20	18	0.75	3.33	0	0	15.0	638 P
K03460_at	9	0	20	20	18	0.45	2.81	0	0	Inf	632 P
D29012_at	12	3	20	20	18	0.60	2.49	0	0	4.0	628 P
D14710_at	15	0	20	20	18	0.75	3.42	2	0	Inf	613 P
D45248_at	14	1	20	20	18	0.70	3.48	0	0	14.0	603 P
M15661_at	17	1	20	20	18	0.85	3.85	0	0	17.0	600 P
HG1153-HT1153_at	13	1	20	20	18	0.65	3.12	0	0	13.0	583 P
D28124_at	14	0	20	20	18	0.70	2.85	0	0	Inf	580 P
J04988_at	14	0	20	20	18	0.70	3.69	1	0	Inf	578 P
AFFX-BioC-5_at	15	1	20	20	18	0.75	2.69	0	0	15.0	557 P
K02765_at	15	0	20	20	18	0.75	2.97	1	0	Inf	540 P
J02854_at	11	0	20	20	18	0.55	2.21	0	0	Inf	522 P
D13118_at	9	1	20	20	18	0.45	2.11	1	0	9.0	501 P
D23662_at	14	1	20	20	18	0.70	2.87	0	0	14.0	496 P
D29863_at	13	1	20	20	18	0.65	2.14	0	0	13.0	482 P
D00761_at	15	0	20	20	18	0.75	2.92	0	0	Inf	462 P
M12529_at	9	1	20	20	18	0.45	2.16	0	0	9.0	448 P
L12168_at	10	0	20	20	18	0.50	2.72	0	0	Inf	445 P
M11119_at	9	0	20	20	18	0.45	1.94	0	0	Inf	437 P
D31883_at	10	2	20	20	18	0.50	1.48	0	0	5.0	431 P
D31846_at	10	0	20	20	18	0.50	1.89	0	0	Inf	424 P
M20471_at	15	0	20	20	18	0.75	2.97	0	0	Inf	421 P
D38548_at	9	1	20	20	18	0.45	2.00	0	0	9.0	417 P
J04456_at	16	0	20	20	18	0.80	3.92	1	0	Inf	413 P
AFFX-HUMGAPDH/M331	12	3	20	20	18	0.60	2.01	0	0	4.0	406 P
HG987-HT987_at	15	3	20	20	18	0.75	3.80	2	0	5.0	404 P
D23673_at	11	0	20	20	18	0.55	2.25	0	0	Inf	401 P
AFFX-BioC-3_at	13	0	20	20	18	0.65	2.46	0	0	Inf	381 P
D14520_at	10	1	20	20	18	0.50	2.04	0	0	10.0	387 P
D26598_at	10	0	20	20	18	0.50	2.32	0	0	Inf	384 P
D16562_at	15	1	20	20	17	0.75	4.14	1	1	15.0	364 P
L15702_at	12	2	20	20	18	0.60	1.91	0	0	8.0	363 P
L3842_msa1_at	14	1	20	20	18	0.70	3.38	0	0	14.0	358 P
L38486_at	12	2	20	20	18	0.60	2.38	0	0	6.0	354 P
D13748_at	12	1	20	20	18	0.60	2.07	0	0	12.0	353 P
HG2855-HT2855_at	13	1	20	20	18	0.65	2.94	0	0	13.0	347 P
AFFX-HSAC07X00351_5	12	0	20	20	17	0.60	3.21	0	0	Inf	346 P
D85815_at	11	3	20	20	18	0.55	1.88	0	0	3.7	344 P

Normal urothelium A

D25274_at	11	2	20	20	17	0.55	2.35	0	0.55	342 P
L21954_at	13	4	20	20	18	0.65	2.18	0	0.33	341 P
D63475_at	14	1	20	20	18	0.70	3.17	0	0.140	338 P
M19483_at	13	1	20	20	18	0.65	2.28	0	0.130	338 P
D85429_at	11	1	20	20	18	0.55	2.03	0	0.110	333 P
D83878_at	12	3	20	20	18	0.60	1.71	0	0.40	331 P
D50310_at	18	0	20	20	18	0.90	3.57	0	0 Inf	325 P
D25068_at	10	2	20	20	18	0.50	2.74	1	0.50	323 P
D13640_at	7	2	20	20	18	0.35	1.74	0	0.35	313 P
M16279_at	7	2	20	20	18	0.35	1.59	0	0.35	311 P
D11428_at	7	1	20	20	18	0.35	1.23	0	1.70	309 P
HG2566-HT4867_at	10	2	20	20	18	0.50	1.69	0	0.50	307 P
AF015910_at	8	0	20	20	18	0.40	1.59	0	0 Inf	306 P
L19605_at	12	1	20	20	17	0.60	2.18	0	0.120	305 P
D80209_at	14	1	20	20	18	0.70	3.13	0	0.140	299 P
D38047_at	11	0	20	20	18	0.55	2.10	0	0 Inf	298 P
J04173_at	9	2	20	20	18	0.45	2.20	0	0.45	287 P
M13955_at	11	3	20	20	18	0.55	1.67	0	0.37	295 P
D49400_at	8	1	20	20	18	0.45	1.94	0	0.90	283 P
L09604_at	10	2	20	20	18	0.50	2.00	0	0.50	282 P
AB000584_at	10	2	20	20	18	0.50	1.42	0	0.50	286 P
L76200_at	10	3	20	20	18	0.50	2.12	1	0.33	285 P
J04611_at	10	1	20	20	17	0.50	1.79	0	0.100	279 P
M14200_ma1_at	10	1	20	20	17	0.50	1.88	0	0.100	274 P
HG1614-HT1614_at	8	1	20	20	17	0.45	1.30	0	0.80	272 P
J04784_at	9	3	20	20	18	0.45	1.45	0	0.30	271 P
AF006084_at	11	2	20	20	17	0.55	2.31	0	0.55	269 P
D26599_at	13	2	20	20	18	0.65	2.75	0	0.65	269 P
D50863_at	13	2	20	20	18	0.85	2.43	0	1.65	269 P
D16217_at	11	0	20	20	17	0.55	2.34	0	0 Inf	267 P
J02874_at	12	2	20	20	18	0.60	3.23	2	0.60	267 P
D25216_at	10	1	20	20	17	0.50	2.07	1	0.100	265 P
D55696_at	9	2	20	20	17	0.45	2.27	1	0.45	260 P
D82348_at	11	2	20	20	18	0.55	2.22	0	0.55	258 P
D14694_at	13	0	20	20	18	0.65	2.55	0	0 Inf	255 P
J03600_at	11	2	20	20	18	0.55	2.56	0	0.55	255 P
J03459_at	10	1	20	20	18	0.50	1.97	1	0.100	254 P
L25080_at	10	2	20	20	18	0.50	2.35	1	0.50	250 P
L07633_at	12	0	20	20	18	0.60	3.26	0	0 Inf	249 P
D10522_at	13	1	20	20	18	0.65	3.23	1	0.130	248 P
L02426_at	11	0	20	20	18	0.55	2.00	0	0 Inf	242 P
L10264_at	13	1	20	20	18	0.65	2.61	0	0.130	239 P
M14050_at	11	0	20	20	18	0.55	2.20	0	0 Inf	235 P
L13977_at	12	1	20	20	18	0.60	2.18	0	0.120	232 P
J03069_ma1_at	9	2	20	20	18	0.45	1.95	0	0.45	230 P
M13755_at	7	1	20	20	18	0.35	1.08	0	0.70	230 P
HG1862-HT1897_at	10	2	20	20	18	0.50	2.50	0	0.50	228 P
L13852_at	7	0	20	20	18	0.35	1.48	0	0 Inf	225 P
M12886_at	11	2	20	20	17	0.55	1.57	0	0.55	222 P
D88422_at	11	2	20	20	18	0.55	2.38	0	0.55	221 P
L25081_at	7	0	20	20	18	0.35	1.12	0	0 Inf	219 P

Side 3

Normal urothelium A

D26600_at	15	1	20	20	17.075	2.67	0	0	15.0	218 P
L11285_at	9	2	20	20	18.045	1.62	0	0	4.5	218 P
L40904_at	7	0	20	20	18.035	1.76	0	0	Inf	218 P
HG3484-HT3688_at	8	1	20	20	17.040	1.31	0	0	8.0	217 P
D21089_at	10	1	20	20	17.050	2.25	1	0	10.0	215 P
D86985_at	8	1	20	20	18.040	1.45	0	0	8.0	215 P
L24203_at	11	0	20	20	18.055	1.98	0	0	Inf	213 P
M14676_at	9	3	20	20	18.045	1.96	0	0	3.0	213 P
K03430_at	8	0	20	20	18.045	1.79	0	0	Inf	212 P
L40027_at	10	2	20	20	18.050	1.97	1	0	5.0	212 P
D00763_at	11	1	20	20	18.055	1.92	0	0	11.0	211 P
L19437_at	10	0	20	20	18.050	2.35	1	0	Inf	210 P
HG1076-HT1078_at	14	2	20	20	18.070	2.55	0	0	7.0	207 P
L32977_at	14	1	20	20	17.070	3.51	1	0	14.0	204 P
D87953_at	11	0	20	20	18.055	2.89	0	0	Inf	203 P
AB001325_at	8	2	20	20	18.040	0.92	0	0	4.0	200 P
D78134_at	10	2	20	20	17.050	2.15	0	0	5.0	200 P
D43642_at	12	1	20	20	18.060	2.32	0	0	12.0	187 P
D14682_at	10	1	20	20	18.050	2.68	1	0	10.0	181 P
D31884_at	11	2	20	20	18.055	1.89	0	0	5.5	191 P
D83542_at	10	3	20	20	18.050	1.53	0	0	3.3	191 P
HG3514-HT3708_at	10	1	20	20	18.050	2.20	0	0	10.0	191 P
D63486_at	8	0	20	20	17.040	1.11	0	0	Inf	190 P
D31890_at	13	1	20	20	17.065	3.06	1	0	13.0	186 P
D49738_at	11	3	20	20	18.055	1.83	0	0	3.7	186 P
D50063_at	9	2	20	20	18.045	1.60	1	1	4.5	183 P
D63160_at	7	0	20	20	18.035	1.23	0	0	Inf	178 P
D38305_at	10	0	20	20	17.050	2.17	1	0	Inf	176 P
D38048_at	11	1	20	20	18.055	2.31	0	0	11.0	173 P
D49387_at	9	1	20	20	18.045	2.24	1	0	9.0	173 P
D31765_at	8	1	20	20	18.040	1.61	0	0	8.0	172 P
M15182_at	8	2	20	20	18.040	1.10	0	0	4.0	171 P
HG4287-HT4567_at	14	2	20	20	18.070	2.88	1	0	7.0	170 P
L12350_at	11	0	20	20	18.055	2.36	0	0	Inf	170 P
D32050_at	8	2	20	20	18.040	1.22	0	0	4.0	168 P
L08246_at	10	2	20	20	18.050	1.49	0	1	5.0	165 P
L28010_at	11	1	20	20	18.055	2.23	0	0	11.0	165 P
M13450_at	13	0	20	20	18.065	2.71	1	0	Inf	165 P
D85245_at	10	2	20	20	18.050	2.05	1	0	5.0	160 P
L11708_at	9	3	20	20	18.045	1.60	0	0	3.0	159 P
D78991_at	7	1	20	20	18.035	1.81	0	0	7.0	158 P
AJ001421_at	10	0	20	20	18.050	1.17	0	0	Inf	157 P
D14043_at	11	1	20	20	17.055	2.52	0	0	11.0	157 P
D13370_at	10	1	20	20	17.050	1.50	0	0	10.0	153 P
K03195_at	10	2	20	20	18.050	2.95	3	0	5.0	153 P
L76465_at	11	3	20	20	18.055	2.43	2	1	3.7	150 P
D84239_at	10	2	20	20	18.050	1.69	0	0	5.0	149 P
D89016_at	8	1	20	20	17.040	1.63	0	0	8.0	145 P
M11717_max1_at	12	3	20	20	18.050	2.87	3	1	4.0	146 P
M11726_at	8	1	20	20	18.040	1.57	0	0	8.0	145 P
L13197_at	7	0	20	20	18.035	1.59	0	0	Inf	144 P

Normal urothelium A

L20773_at	10	3	20	20	18	0.50	1.40	0	0.33	144 P
HG2614-HT2710_at	7	1	20	20	18	0.35	1.29	0	0.70	143 P
L36531_at	9	1	20	20	18	0.45	1.05	0	0.90	142 P
D14686_at	9	2	20	20	18	0.45	1.25	0	0.45	141 P
D55554_at	9	1	20	20	17	0.45	1.51	0	0.90	141 P
HG1102-HT1102_at	7	1	20	20	18	0.35	1.71	0	0.70	140 P
L11669_at	11	2	20	20	17	0.55	1.37	0	0.55	138 P
L38698_at	7	1	20	20	18	0.35	1.20	0	0.70	138 P
L41559_at	8	2	20	20	18	0.40	1.47	0	0.40	138 P
D50911_at	9	2	20	20	18	0.45	1.29	0	0.45	136 P
D38076_at	7	1	20	20	18	0.35	1.43	0	0.70	134 P
D88978_at	13	2	20	20	18	0.65	2.94	2	1.65	133 P
L34587_at	9	1	20	20	18	0.45	1.38	0	0.90	133 P
AF006041_at	11	3	20	20	18	0.55	1.49	0	0.37	132 P
D80276_at	8	1	20	20	18	0.40	1.48	0	0.80	132 P
HG960-HT960_at	10	1	20	20	18	0.50	1.38	0	0.10.0	132 P
L38064_rna1_at	9	2	20	20	18	0.45	1.38	0	0.45	132 P
AC002045_xpt1_at	8	0	20	20	18	0.40	1.50	0	0.1nf	128 P
D50912_at	8	1	20	20	18	0.40	1.42	0	0.80	127 P
D87438_at	8	2	20	20	17	0.40	1.58	0	0.40	127 P
D28915_at	11	0	20	20	18	0.55	2.33	1	0.1nf	125 P
HG1602-HT1602_at	7	1	20	20	18	0.35	0.98	0	0.70	124 P
D21260_at	8	0	20	20	17	0.40	1.58	0	0.1nf	123 P
D83478_at	9	0	20	20	17	0.45	2.17	1	0.1nf	123 P
D80005_at	8	2	20	20	18	0.40	1.84	0	0.40	123 P
D84110_at	14	1	20	20	17	0.70	2.96	2	0.14.0	123 P
.06132_at	9	3	20	20	18	0.45	2.09	2	0.30	122 P
.087258_at	9	2	20	20	18	0.45	1.61	0	0.45	121 P
.01396_at	12	2	20	20	18	0.60	1.50	0	0.60	121 P
.07033_at	10	2	20	20	18	0.50	1.90	0	0.50	121 P
.29843_at	10	3	20	20	18	0.50	1.96	1	0.33	120 P
D50683_at	13	1	20	20	18	0.65	2.42	0	0.13.0	120 P
D85758_at	9	3	20	20	17	0.45	1.94	2	0.30	119 P
L19779_at	7	1	20	20	18	0.35	1.34	0	0.70	118 P
L27709_at	12	2	20	20	18	0.60	3.22	1	0.60	118 P
L40393_at	9	1	20	20	18	0.45	2.17	2	0.90	118 P
D83032_at	7	2	20	20	18	0.35	1.81	3	1.35	117 P
D30755_at	7	2	20	20	18	0.35	1.53	0	0.35	116 P
D49488_at	14	2	20	20	18	0.70	3.79	3	0.70	116 P
D83782_at	7	2	20	20	18	0.35	1.58	1	0.35	116 P
D56495_at	8	0	20	20	18	0.40	1.57	0	0.1nf	115 P
M13207_at	8	2	20	20	18	0.40	0.91	0	0.40	115 P
D87673_at	7	1	20	20	17	0.35	0.94	0	0.70	114 P
M11437_cds2_at	8	0	20	20	18	0.40	2.10	1	0.1nf	114 P
D21862_at	12	2	20	20	18	0.60	2.95	2	0.60	113 P
L19183_at	8	2	20	20	18	0.40	1.49	0	0.40	113 P
L77888_at	12	4	20	20	18	0.80	2.61	1	0.30	113 P
M18079_at	10	2	20	20	18	0.50	1.91	1	0.50	113 P
D43960_at	7	1	20	20	18	0.35	1.79	0	0.70	111 P
D14658_at	8	1	20	20	18	0.40	1.69	0	0.80	110 P
M18737_rna1_at	8	2	20	20	18	0.40	1.29	1	0.40	110 P

Normal urothelium A

D78611_at	10	1	20	20	18.050	1.91	1	0	10.0	109 P
L49168_at	10	0	20	20	17.050	1.50	0	0	Inf	109 P
D00760_at	10	1	20	20	18.050	1.53	0	0	10.0	107 P
L08666_at	8	2	20	20	17.040	1.26	0	0	4.0	107 P
AB000115_at	7	1	20	20	18.035	0.97	0	0	7.0	106 P
D79986_at	9	1	20	20	18.045	1.89	1	0	9.0	106 P
D86957_at	12	2	20	20	17.060	2.67	1	1	6.0	106 P
D14663_at	9	0	20	20	18.045	2.11	0	0	Inf	105 P
D42043_at	11	3	20	20	18.055	2.49	0	0	3.7	104 P
M12759_at	9	1	20	20	18.045	1.95	1	0	8.0	104 P
HG3510-HT3704_at	9	0	20	20	18.045	1.50	0	0	Inf	103 P
D90086_at	10	1	20	20	18.050	2.04	1	0	10.0	102 P
D79994_at	8	1	20	20	18.040	1.46	0	0	8.0	101 P
HG4058-HT4328_at	10	3	20	20	18.050	1.62	1	0	3.3	100 P
L21936_at	8	0	20	20	18.040	2.02	1	0	Inf	100 P
M11716_at	8	0	20	20	18.040	1.43	0	0	Inf	100 P
D84454_at	7	1	20	20	18.035	1.27	0	0	7.0	99 P
D21851_at	9	2	20	20	18.045	1.69	1	0	4.5	99 P
HG2274-HT2370_at	8	1	20	20	17.040	1.34	0	0	8.0	98 P
HG4073-HT4343_at	7	1	20	20	18.035	1.22	0	0	7.0	98 P
HG4243-HT4513_at	11	2	20	20	18.055	1.92	1	0	5.5	97 P
HG908-HT908_at	8	1	20	20	18.045	2.06	0	0	9.0	97 P
HG1879-HT1918_at	8	0	20	20	18.045	2.15	1	0	Inf	96 P
L41658_mn1_at	7	1	20	20	17.035	1.22	0	0	7.0	96 P
D50640_at	13	2	20	20	18.065	2.89	2	0	6.5	95 P
HG1869-HT1904_at	9	1	20	20	18.045	1.41	0	0	9.0	95 P
HG2167-HT2237_at	10	2	20	20	18.050	1.82	0	0	5.0	95 P
L13391_at	11	0	20	20	18.055	2.08	0	0	Inf	95 P
L16942_at	8	1	20	20	18.040	0.91	0	0	8.0	95 P
D44466_at	10	1	20	20	18.050	1.47	0	0	10.0	94 P
D49488_at	11	3	20	20	18.055	2.45	1	0	3.7	92 P
D85181_at	11	3	20	20	18.055	2.17	1	0	3.7	92 P
D14878_at	10	2	20	20	18.050	1.95	0	0	5.0	91 P
D86962_at	12	4	20	20	18.060	1.83	0	1	3.0	91 P
D21853_at	7	1	20	20	18.035	1.41	1	0	7.0	90 P
D38549_at	10	3	20	20	17.050	2.39	2	0	3.3	89 P
D84294_at	10	2	20	20	18.050	2.10	2	1	5.0	89 P
D87435_at	8	2	20	20	18.040	1.46	0	0	4.0	89 P
D25278_at	11	2	20	20	17.055	2.02	1	0	5.5	88 P
D79996_at	10	3	20	20	18.050	1.52	1	0	3.3	88 P
L12535_at	8	1	20	20	18.045	3.21	3	0	9.0	88 P
D63480_at	8	1	20	20	18.040	1.90	0	0	6.0	87 P
D79995_at	7	0	20	20	18.035	1.31	0	0	Inf	87 P
L19314_at	7	1	20	20	17.035	1.39	1	0	7.0	87 P
L42378_at	9	3	20	20	18.045	1.74	0	0	3.0	86 P
D30756_at	10	3	20	20	18.050	1.78	2	0	3.3	84 P
D50857_at	8	2	20	20	18.040	1.48	0	0	4.0	84 P
HG1112-HT1112_at	8	0	20	20	17.040	1.25	0	0	Inf	82 P
D83004_at	8	2	20	20	18.040	0.98	0	0	4.0	80 P

Side 6

Normal urothelium A

D876B4_at	10	2	20	20	18.0.50	2.64	3	0.5.0	80 P
HG2096-HT114_at	8	1	20	20	18.0.40	1.45	0	0.8.0	78 P
L29008_at	9	3	20	20	18.0.45	1.64	1	0.3.0	78 P
D28641_at	9	1	20	20	18.0.45	2.71	3	0.9.0	77 P
L18972_at	7	1	20	20	18.0.35	1.12	0	0.7.0	77 P
J04056_at	10	3	20	20	17.0.50	1.73	0	0.3.3	76 P
L40836_at	7	2	20	20	18.0.35	1.43	0	1.3.5	76 P
L24470_at	7	1	20	20	18.0.35	0.96	0	0.7.0	75 P
L40357_at	9	2	20	20	18.0.45	1.40	0	1.4.5	75 P
L27560_at	9	2	20	20	18.0.45	1.59	1	0.4.5	74 P
D13639_at	9	2	20	20	18.0.45	1.59	0	0.4.5	70 P
L43631_at	8	2	20	20	18.0.40	1.65	1	0.4.0	70 P
D28476_at	8	1	20	20	18.0.40	1.63	0	0.8.0	69 P
D42123_at	7	1	20	20	18.0.35	1.11	0	0.7.0	69 P
D88613_at	9	2	20	20	17.0.45	1.98	2	0.4.5	68 P
D17400_at	9	1	20	20	18.0.45	1.53	0	0.9.0	67 P
AF012270_at	9	1	20	20	18.0.45	1.39	0	0.9.0	65 P
D50827_at	9	2	20	20	18.0.45	1.48	0	0.4.5	85 P
D38521_at	8	2	20	20	17.0.40	1.30	1	0.4.0	64 P
D38553_at	7	2	20	20	18.0.35	1.61	0	0.3.5	64 P
D80006_at	8	1	20	20	18.0.40	2.01	1	0.8.0	64 P
L42542_at	8	1	20	20	17.0.40	1.09	0	0.8.0	63 P
D14695_at	11	2	20	20	18.0.55	1.49	0	0.5.5	62 P
L78703_at	8	2	20	20	18.0.40	1.61	2	0.4.0	62 P
HG4336-HT4606_at	9	2	20	20	18.0.45	1.91	0	0.4.5	61 P
D50917_at	11	3	20	20	18.0.55	2.24	2	1.3.7	58 P
D86985_at	12	3	20	20	18.0.60	1.04	0	1.4.0	58 P
HG4390-HT4660_at	8	1	20	20	18.0.40	1.15	0	0.8.0	58 P
L33881_at	12	4	20	20	18.0.60	1.80	1	0.3.0	58 P
D80004_at	7	1	20	20	17.0.35	1.02	0	0.7.0	57 P
D43767_at	8	2	20	20	17.0.40	0.90	0	0.4.0	55 P
D50525_at	9	2	20	20	17.0.45	2.21	3	0.4.5	55 P
L76380_at	11	3	20	20	18.0.55	1.80	0	0.3.7	55 P
D42087_at	9	3	20	20	18.0.45	2.32	2	1.3.0	54 P
HG2460-HT2556_at	9	3	20	20	18.0.45	1.85	2	0.3.0	50 P
L07515_at	8	2	20	20	18.0.40	1.10	0	0.4.0	50 P
L20581_at	8	2	20	20	18.0.40	1.30	0	2.4.0	50 P
L77563_at	7	2	20	20	18.0.35	1.68	2	0.3.5	50 P
D63412_at	8	1	20	20	18.0.40	1.08	0	0.8.0	48 P
J04162_at	7	2	20	20	18.0.35	1.57	0	0.3.5	48 P
D15050_at	8	1	20	20	17.0.40	0.97	0	0.8.0	45 P
L10123_at	10	2	20	20	18.0.50	2.00	2	0.5.0	45 P
AFFX-HUMISGF3AM978	9	3	20	20	18.0.45	1.96	0	0.3.0	44 P
L32163_at	9	3	20	20	18.0.40	1.79	1	0.4.0	42 P
D14664_at	9	3	20	20	18.0.45	1.51	1	1.3.0	41 P
D86425_at	9	3	20	20	18.0.45	2.58	2	0.3.0	37 P
L11885_at	8	2	20	20	18.0.45	1.08	0	0.4.5	34 P
D63875_at	9	2	20	20	18.0.45	1.25	0	0.4.5	29 P
L40388_at	9	1	20	20	18.0.45	1.79	0	0.9.0	23 P
D87443_at	7	2	20	20	18.0.35	1.71	1	0.3.5	22 P

Normal urothelium B

Gene Name	Positive	Negative	Paired	Paired	Log Avg	PM Ex	MMI	Pos	Neg	Avg Diff	Abs Call
hum_allu_at	69	0	69	69	7.55	14	0	Inf	34085 P		
U14973_at	18	0	20	20	18.90	1	0	Inf	6948 P		
AFFX-CreX-3_at	19	1	20	20	18.95	0	0	18.0	5673 P		
U14969_at	20	0	20	20	18.100	1	0	Inf	5259 P		
U14972_at	19	0	20	20	18.035	0	0	Inf	5247 P		
M24194_at	18	0	20	20	18.095	0	0	Inf	4955 P		
M81757_at	18	0	20	20	18.090	1	0	Inf	4759 P		
U14968_at	16	0	20	20	18.080	2	0	Inf	4708 P		
U12465_at	20	0	20	20	18.100	0	0	Inf	4503 P		
M31951_at	15	3	20	20	18.075	7	0	5.0	4128 P		
AFFX-CreX-5_at	20	0	20	20	18.100	1	0	Inf	3983 P		
M60854_at	18	0	20	20	18.090	4	0	Inf	3548 P		
S79522_at	17	0	20	20	18.085	2	0	Inf	3543 P		
M84711_at	17	0	20	20	18.085	0	0	Inf	3365 P		
M64716_at	14	3	20	20	18.070	1	0	4.7	3345 P		
AFFX-HUNGAPDH33197_3	19	0	20	20	17.095	1	0	Inf	3257 P		
M77232_mai1_at	18	1	20	20	18.080	1	0	16.0	3217 P		
AFFX-HSAC07X00351_3_at	16	0	20	20	18.080	4	0	Inf	3110 P		
U49869_mai1_at	19	0	20	20	17.095	2	0	Inf	3081 P		
U58682_at	17	1	20	20	18.085	2	0	17.0	3033 P		
U14971_at	18	0	20	20	18.090	0	0	Inf	2924 P		
U09953_at	18	0	20	20	18.080	3	0	Inf	2871 P		
U14970_at	18	0	20	20	18.090	2	0	Inf	2723 P		
U12404_at	18	0	20	20	18.080	1	0	Inf	2655 P		
M31520_at	17	0	20	20	18.085	1	0	Inf	2526 P		
M32405_at	11	3	20	20	18.055	1	0	3.7	2461 P		
M33680_at	17	0	20	20	18.085	2	0	Inf	2367 P		
M84526_at	13	0	20	20	18.065	0	0	Inf	2281 P		
AFFX-BioDn-3_at	15	2	20	20	17.075	0	0	7.5	2202 P		
U25789_at	17	1	20	20	18.085	0	0	17.0	2092 P		
S73591_at	15	0	20	20	18.075	1	0	Inf	1714 P		
U15008_at	13	2	20	20	18.065	0	0	6.5	1556 P		
M26880_at	15	0	20	20	18.075	2	0	Inf	1454 P		
U31875_at	18	0	20	20	18.080	0	0	Inf	1358 P		
AFFX-HSAC07X00351_M_at	15	1	20	20	18.075	0	0	15.0	1261 P		
M63138_at	8	1	20	20	18.040	0	0	8.0	1215 P		
M63378_at	15	0	20	20	18.075	1	0	Inf	1169 P		
M57710_at	17	0	20	20	17.085	0	0	Inf	1035 P		
U50523_at	13	3	20	20	18.065	1	1	4.3	946 P		
M95787_at	12	0	20	20	18.060	0	0	Inf	944 P		
AFFX-HSAC07X00351_5_at	13	1	20	20	18.065	0	0	13.0	943 P		
M27891_at	11	2	20	20	18.055	0	0	5.5	943 P		
U21831_at	14	0	20	20	17.070	3	0	Inf	866 P		
U44839_at	11	3	20	20	18.055	0	0	3.7	805 P		
M23613_at	11	2	20	20	18.055	0	0	5.5	779 P		
M34182_at	12	2	20	20	18.060	0	0	6.0	772 P		
U46692_mai1_at	13	2	20	20	18.065	0	0	6.5	748 P		
U37690_at	12	0	20	20	18.060	0	0	Inf	688 P		
M80563_at	11	0	20	20	18.055	0	0	Inf	678 P		
U41835_at	8	1	20	20	18.040	0	0	8.0	658 P		

Side 1

Normal urothelium B

U46751_at	10	2	20	20	18.0.50	2.76	1	0.5.0	644 P
U03057_at	8	2	20	20	18.0.40	1.23	0	0.4.0	643 P
S65738_at	14	1	20	20	18.0.70	3.33	0	0.14.0	621 P
S77356_at	13	3	20	20	18.0.65	2.78	0	0.4.3	615 P
AFFX-HUMGAPDH/M33187_A	12	3	20	20	17.0.60	2.00	0	0.4.0	614 P
U62739_at	10	2	20	20	18.0.50	1.85	0	0.5.0	612 P
S75463_at	9	2	20	20	18.0.45	1.83	1	0.4.5	598 P
U62982_at	11	2	20	20	18.0.55	2.04	0	0.5.5	595 P
M35878_at	12	3	20	20	18.0.60	1.70	0	1.4.0	577 P
U46570_at	8	1	20	20	18.0.40	1.28	0	0.8.0	550 P
AFFX-HUMGAPDH/M33187_5	12	0	20	20	18.0.60	2.95	0	0. Inf	539 P
U11851_at	10	2	20	20	18.0.50	1.58	0	0.5.0	536 P
M57567_at	10	1	20	20	18.0.50	1.70	0	0.10.0	525 P
U01212_at	10	2	20	20	18.0.50	1.25	0	0.5.0	517 P
U03398_at	10	3	20	20	18.0.50	2.46	2	0.3.3	500 P
U45975_at	7	2	20	20	18.0.35	1.31	0	0.3.5	485 P
U46498_at	10	3	20	20	17.0.50	1.65	0	0.3.3	484 P
M76378_at	8	2	20	20	18.0.40	1.16	0	0.4.0	478 P
M55593_at	10	1	20	20	18.0.50	2.09	1	0.10.0	471 P
U09117_at	7	2	20	20	18.0.35	1.38	0	0.3.5	464 P
U46025_at	11	2	20	20	18.0.55	1.76	1	0.5.5	463 P
U51478_at	13	1	20	20	18.0.65	3.39	0	0.13.0	459 P
M28877_at	10	0	20	20	18.0.50	1.79	1	0. Inf	457 P
M32053_at	9	1	20	20	18.0.45	1.90	0	0.9.0	452 P
AFFX-BioC-5_at	8	1	20	20	18.0.40	1.19	0	0.8.0	434 P
U08813_at	12	1	20	20	18.0.60	2.90	0	0.12.0	434 P
M87815_at	9	2	20	20	18.0.45	1.38	0	0.4.5	431 P
M88279_at	11	0	20	20	18.0.55	2.28	0	0. Inf	428 P
S73149_at	8	1	20	20	18.0.40	1.14	0	0.8.0	424 P
M84349_at	11	2	20	20	18.0.55	2.40	0	0.5.5	415 P
U29656_at	7	0	20	20	18.0.35	1.70	0	0. Inf	412 P
U37689_at	10	0	20	20	18.0.50	1.42	0	0. Inf	408 P
M22382_at	9	0	20	20	18.0.45	1.45	0	0. Inf	396 P
S68516_at	8	2	20	20	18.0.40	1.37	0	0.4.0	391 P
M85400_at	11	1	20	20	18.0.55	2.44	1	0.11.0	387 P
U57342_at	9	1	20	20	18.0.45	1.93	0	0.9.0	387 P
M60858_ma1_at	10	2	20	20	18.0.50	2.42	0	0.5.0	376 P
AFFX-BioOn-5_at	8	0	20	20	18.0.45	1.37	0	0. Inf	373 P
M84332_at	10	1	20	20	18.0.50	1.49	0	0.10.0	370 P
M38590_at	10	0	20	20	18.0.50	2.51	1	0. Inf	367 P
M22538_at	7	0	20	20	18.0.35	1.00	0	0. Inf	365 P
U57450_at	10	0	20	20	18.0.50	1.17	0	0. Inf	365 P
U30825_at	11	3	20	20	18.0.55	1.59	0	0.3.7	355 P
M75126_at	9	1	20	20	18.0.45	1.67	0	0.9.0	347 P
M95627_at	7	0	20	20	18.0.35	1.50	0	0. Inf	344 P
U50136_ma1_at	8	2	20	20	18.0.40	1.16	0	0.4.0	338 P
U14603_at	12	0	20	20	18.0.80	2.58	0	0. Inf	337 P
M75099_at	9	0	20	20	18.0.45	2.03	0	0. Inf	338 P
U33821_at	10	1	20	20	18.0.50	1.67	0	0.10.0	336 P
U21128_at	12	3	20	20	18.0.60	2.20	1	1.4.0	327 P
M28713_at	7	1	20	20	18.0.35	1.35	0	0.7.0	324 P
U37519_at	7	2	20	20	18.0.35	1.88	0	0.3.5	321 P

Side 2

Normal urothelium B									
M73547_at	12	4	20	20	18.060	2.03	1	0.30	318 P
M95803_at	12	2	20	20	18.060	1.31	0	1.80	310 P
U41371_at	12	1	20	20	18.060	2.45	0	0.12.0	310 P
AFFX-HSAC07X00351_3_at	13	0	20	20	17.065	2.19	0	0 Inf	303 P
M94345_at	10	2	20	20	18.050	1.48	0	0.50	302 P
U02493_at	8	0	20	20	18.040	1.74	0	0 Inf	302 P
M58285_at	8	0	20	20	18.040	1.16	0	0 Inf	293 P
U02570_at	7	1	20	20	18.035	1.53	0	0.70	283 P
AFFX-BloC_3_at	7	1	20	20	18.035	1.33	0	0.70	292 P
M62831_at	8	0	20	20	18.040	1.16	0	0 Inf	281 P
U32944_at	13	1	20	20	18.065	3.00	2	0.13.0	290 P
U52522_at	7	2	20	20	18.035	1.74	0	0.35	298 P
M88338_at	7	1	20	20	18.035	0.87	0	0.70	283 P
M77349_at	14	0	20	20	18.070	2.49	0	0 Inf	277 P
U29607_at	13	3	20	20	18.065	2.26	2	1.43	276 P
M31303_maf1_at	9	2	20	20	18.045	1.63	0	0.45	274 P
M66439_at	11	1	20	20	18.055	2.84	2	0.11.0	271 P
M63959_at	10	2	20	20	18.050	1.26	0	0.50	270 P
M24899_at	10	2	20	20	18.050	1.58	0	0.50	269 P
U07857_at	13	2	20	20	17.065	2.51	0	1.65	269 P
U30888_at	10	2	20	20	18.050	1.49	0	0.50	266 P
M81780_cds5_at	8	1	20	20	18.040	1.13	0	0.80	258 P
M23254_at	11	3	20	20	17.055	1.84	0	0.37	256 P
U05658_at	10	2	20	20	18.050	1.74	1	1.50	256 P
U49785_at	12	1	20	20	18.060	2.29	0	0.12.0	256 P
U10323_at	10	1	20	20	17.050	2.08	0	0.10.0	254 P
M64347_at	7	1	20	20	18.035	1.70	2	1.70	253 P
U20285_at	9	2	20	20	18.045	1.32	0	0.45	246 P
U43286_at	11	0	20	20	18.055	2.55	1	0 Inf	246 P
M82809_at	13	1	20	20	18.065	2.26	0	0.13.0	243 P
M96856_at	10	3	20	20	18.050	2.22	1	0.33	243 P
U56637_at	7	2	20	20	17.035	1.37	0	1.35	240 P
U40890_at	7	0	20	20	18.035	1.09	0	0 Inf	238 P
U48092_at	8	2	20	20	18.040	0.93	0	0.40	227 P
M91029_cds2_at	7	2	20	20	18.035	1.32	0	0.35	224 P
U52100_at	7	1	20	20	18.035	1.25	0	0.70	224 P
U40998_at	8	2	20	20	18.040	1.32	0	0.40	224 P
M90299_at	8	2	20	20	18.040	1.20	0	0.40	220 P
S71824_at	7	1	20	20	18.035	1.30	0	0.70	220 P
M31627_at	11	2	20	20	18.055	1.69	0	0.55	219 P
M83751_at	7	2	20	20	17.035	1.46	0	0.35	219 P
U43077_at	8	1	20	20	18.040	1.58	0	0.80	215 P
M28980_at	10	2	20	20	18.050	1.52	2	0.50	215 P
M92449_at	10	2	20	20	18.050	1.94	1	0.50	212 P
M28536_at	11	2	20	20	18.055	1.95	0	0.55	207 P
S81083_cds1_at	7	1	20	20	18.035	1.07	0	0.70	207 P
M81601_at	7	1	20	20	18.035	1.55	0	0.70	205 P
U50535_at	11	3	20	20	18.055	2.10	0	0.37	203 P
M87284_at	9	2	20	20	18.045	1.41	0	0.45	202 P
U24152_at	7	2	20	20	18.035	1.43	0	0.35	199 P
U51678_at	10	3	20	20	18.050	1.77	0	0.33	189 P
M64571_at	9	2	20	20	18.045	1.43	0	0.45	187 P

Side 3

Normal urothelium B

574017_at	10	2	20	20	20	18 0.50	1.59	0	0.50	195 P
U38846_at	8	1	20	20	20	18 0.40	1.39	0	0.80	196 P
M32313_at	9	1	20	20	20	18 0.45	1.62	1	0.90	194 P
U43148_at	8	1	20	20	20	18 0.40	1.08	0	0.80	191 P
M55543_at	8	2	20	20	20	18 0.40	1.53	0	0.40	189 P
U37122_at	9	2	20	20	20	17 0.45	1.45	0	0.45	188 P
M37245_at	10	1	20	20	20	18 0.50	1.81	0	0.10.0	186 P
U34962_at	8	1	20	20	20	18 0.45	1.53	0	0.90	186 P
M94556_at	10	3	20	20	20	18 0.50	1.78	1	0.33	183 P
M31013_at	11	2	20	20	20	17 0.55	2.34	1	0.55	175 P
U15174_at	7	1	20	20	20	18 0.35	1.30	0	1.70	173 P
M84856_at	8	1	20	20	20	18 0.40	1.08	1	0.80	172 P
U00952_at	9	1	20	20	20	17 0.45	2.14	0	0.90	170 P
U14193_at	8	2	20	20	20	18 0.40	1.48	0	0.40	170 P
U40343_at	7	1	20	20	20	18 0.35	1.29	0	0.70	170 P
U02020_at	9	3	20	20	20	18 0.45	2.42	1	0.30	168 P
U36764_at	10	3	20	20	20	18 0.50	1.60	1	0.33	167 P
M86667_at	9	3	20	20	20	18 0.45	1.42	0	0.30	166 P
S69115_at	7	1	20	20	20	18 0.35	2.01	1	0.70	165 P
M29971_at	8	1	20	20	20	18 0.40	0.94	0	0.80	165 P
U19937_at	7	2	20	20	20	18 0.35	1.54	0	1.35	164 P
U31384_at	8	2	20	20	20	18 0.40	1.12	0	0.40	161 P
S83364_at	9	2	20	20	20	18 0.45	1.55	0	0.45	159 P
U54778_at	9	3	20	20	20	18 0.45	1.93	1	0.30	159 P
U03485_at	7	0	20	20	20	18 0.35	0.91	0	Inf	158 P
M74002_at	7	1	20	20	20	18 0.35	1.06	0	0.70	157 P
U20325_at	7	2	20	20	20	18 0.35	1.74	1	0.35	157 P
M80629_at	11	1	20	20	20	18 0.55	1.58	0	0.11.0	156 P
U20582_at	7	1	20	20	20	18 0.35	1.01	0	0.70	154 P
U27185_at	9	2	20	20	20	18 0.45	1.57	0	0.45	152 P
U57721_at	10	1	20	20	20	18 0.50	2.47	1	0.10.0	150 P
M34423_at	8	1	20	20	20	18 0.40	1.03	0	0.80	149 P
U47742_at	8	1	20	20	20	17 0.40	1.12	0	0.80	149 P
U34252_at	10	3	20	20	20	18 0.50	2.26	2	0.33	148 P
U30899_at	9	3	20	20	20	17 0.45	1.48	0	0.30	146 P
U53446_at	9	2	20	20	20	18 0.45	1.43	0	0.45	145 P
S81419_at	7	2	20	20	20	18 0.35	1.38	0	0.35	143 P
U31383_at	9	3	20	20	20	18 0.45	1.62	1	0.30	142 P
U29680_at	8	2	20	20	20	18 0.40	1.47	0	0.40	139 P
M58603_at	8	2	20	20	20	18 0.40	1.01	0	0.40	138 P
M83425_at	9	1	20	20	20	18 0.45	1.39	0	0.90	137 P
U21049_at	9	1	20	20	20	18 0.45	1.31	0	0.90	130 P
U58919_at	9	2	20	20	20	18 0.45	1.33	0	0.45	128 P
S76965_at	8	1	20	20	20	18 0.40	2.11	0	0.80	123 P
M28879_at	9	2	20	20	20	18 0.45	1.50	2	0.45	122 P
U15782_at	7	2	20	20	20	18 0.35	1.53	1	0.35	122 P
M85276_at	8	2	20	20	20	18 0.40	0.90	0	0.40	120 P
U03888_at	8	1	20	20	20	18 0.40	1.65	0	0.80	116 P
U28249_at	7	1	20	20	20	18 0.35	1.69	1	0.70	115 P
U09316_at	9	3	20	20	20	18 0.45	1.62	0	0.30	113 P
U07158_at	8	2	20	20	20	18 0.40	1.19	1	1.40	111 P
U40369_ma1_at	9	2	20	20	20	18 0.45	1.75	0	1.45	111 P

Side 4

Normal urothelium B									
U49352_at	12	3	20	20	18 0.60	2.61	2	0 4.0	111 P
U59423_at	7	2	20	20	18 0.35	1.31	0	0 3.5	107 P
M65131_ma1_at	7	1	20	20	18 0.35	1.23	0	0 7.0	102 P
U09412_at	8	2	20	20	18 0.40	1.05	0	0 4.0	98 P
U50928_at	11	1	20	20	18 0.55	1.92	1	1 11.0	98 P
U49114_at	10	3	20	20	18 0.50	1.51	1	0 3.3	95 P
U02632_at	9	2	20	20	18 0.45	1.22	0	0 4.5	90 P
U19345_at	7	1	20	20	18 0.35	1.53	0	0 7.0	87 P
U53003_at	9	3	20	20	18 0.45	1.78	1	0 3.0	82 P
U13816_at	9	3	20	20	18 0.45	1.45	2	1 3.0	78 P
U47054_at	7	2	20	20	18 0.35	1.58	2	0 3.5	78 P
M23161_at	8	1	20	20	18 0.40	1.14	0	0 8.0	77 P
M80686_at	9	1	20	20	18 0.45	1.46	2	0 8.0	76 P
U46752_at	8	2	20	20	18 0.40	1.14	0	0 4.0	76 P
U03058_at	7	2	20	20	18 0.35	1.44	2	0 3.5	70 P
U28386_at	9	2	20	20	18 0.45	1.66	1	0 4.5	69 P
U55766_at	7	1	20	20	18 0.35	0.98	0	1 7.0	59 P
U09367_at	8	2	20	20	18 0.40	0.92	0	0 4.0	67 P
U31116_at	7	2	20	20	18 0.35	1.42	1	0 3.5	67 P
U35735_at	7	1	20	20	18 0.35	1.17	0	0 7.0	65 P
U05875_at	7	2	20	20	18 0.35	1.52	0	0 3.5	37 P

Gene Name	Normal urothelium C																	
	Positive	Negative	Pairs	Pairs	Usat	Pairs	InAv	Pos	Fract	Log	Avg	PM	Exces	MM	Exces	Pos/Neg	Avg Diff	Abs Call
hurr_atu_at	69	0	69	69	69	69	67	1.00	7.20				9	0	Inf		22212	P
Z12982_at	18	0	20	20	20	20	18	0.90	7.43				5	0	Inf		11237	P
X56932_at	20	0	20	20	20	20	18	1.00	8.65				9	0	Inf		8427	P
Z70759_at	20	0	20	20	20	20	18	1.00	8.49				8	0	Inf		8169	P
X69150_at	19	0	20	20	20	20	18	0.95	7.61				8	0	Inf		6897	P
X15940_at	19	0	20	20	20	20	18	0.95	7.00				4	0	Inf		5994	P
X06617_at	20	0	20	20	20	20	18	1.00	6.37				1	0	Inf		5392	P
X03342_at	20	0	20	20	20	20	18	1.00	7.66				5	0	Inf		5147	P
AFFX-CreX-3_at	19	0	20	20	20	20	18	0.95	8.47				6	0	Inf		4809	P
X17206_at	19	0	20	20	20	20	18	0.95	7.56				6	0	Inf		4634	P
X64707_at	15	0	20	20	20	20	18	0.75	6.10				3	0	Inf		4230	P
Z23090_at	17	0	20	20	20	20	18	0.85	5.02				0	0	Inf		4116	P
X62691_at	20	0	20	20	20	20	18	1.00	7.40				3	0	Inf		4105	P
X65814_at	20	0	20	20	20	20	18	1.00	7.02				2	0	Inf		4027	P
AB002533_at	19	0	20	20	20	20	18	0.95	6.88				4	0	Inf		4012	P
X16064_at	17	0	20	20	20	20	18	0.85	7.60				4	0	Inf		3795	P
X63527_at	20	0	20	20	20	20	18	1.00	7.94				9	0	Inf		3755	P
X55954_at	20	0	20	20	20	20	18	1.00	7.24				4	0	Inf		3744	P
AFFX-CreX-5_at	20	0	20	20	20	20	18	1.00	8.02				5	0	Inf		3538	P
X80822_at	18	0	20	20	20	20	18	0.90	5.48				0	0	Inf		3471	P
X67247_ma1_at	20	0	20	20	20	20	17	1.00	8.00				6	0	Inf		3402	P
Z26876_at	19	0	20	20	20	20	18	0.95	7.54				5	0	Inf		3163	P
X73460_at	19	0	20	20	20	20	18	0.95	6.44				4	0	Inf		3009	P
X53777_at	18	1	20	20	20	20	18	0.90	7.48				6	0	18.0		2851	P
X78234_at	20	0	20	20	20	20	18	1.00	7.48				3	0	Inf		2843	P
AFFX-HSAC07X00351_3_at	19	0	20	20	20	20	18	0.95	6.48				2	0	Inf		2664	P
X69391_at	20	0	20	20	20	20	18	1.00	6.86				4	0	Inf		2656	P
AFFX-BioDn-3_at	18	0	20	20	20	20	18	0.90	5.07				0	0	Inf		2613	P
Z28407_at	15	1	20	20	20	20	18	0.75	4.43				1	0	15.0		2557	P
AFFX-HUMGAPDH/M33197_3_a	19	0	20	20	20	20	17	0.95	5.41				0	0	Inf		2535	P
U76027_rna3_at	18	2	20	20	20	20	18	0.90	7.15				4	0	9.0		2430	P
Z25749_ma1_at	16	1	20	20	20	20	18	0.80	5.44				2	0	16.0		2348	P
X00274_at	20	0	20	20	20	20	16	1.00	8.13				7	0	Inf		2334	P
X65997_rna1_at	19	0	20	20	20	20	18	0.95	5.12				2	0	Inf		2279	P
Y00705_at	18	0	20	20	20	20	18	0.90	7.34				5	0	Inf		2124	P
:55715_at	17	0	20	20	20	20	18	0.85	5.96				2	0	Inf		1884	P
07755_at	18	0	20	20	20	20	18	0.90	6.05				0	0	Inf		1877	P
52966_at	15	2	20	20	20	20	17	0.75	5.36				2	0	7.5		1485	P
:52851_rna1_at	20	0	20	20	20	20	18	1.00	6.46				1	0	Inf		1384	P
:15183_at	17	2	20	20	20	20	18	0.85	5.76				2	1	8.5		1273	P
X83036_at	16	0	20	20	20	20	18	0.80	5.04				3	0	Inf		1232	P
X95404_at	14	0	20	20	20	20	18	0.70	4.70				2	0	Inf		1170	P
X57959_at	19	0	20	20	20	20	17	0.95	7.19				3	0	Inf		1125	P
X15341_at	19	0	20	20	20	20	18	0.85	6.40				0	0	Inf		1071	P
AFFX-HSAC07X00351_M_at	16	1	20	20	20	20	18	0.80	4.07				0	0	16.0		1036	P
Y00433_at	14	0	20	20	20	20	18	0.70	4.15				0	0	Inf		1027	P
X60489_at	17	0	20	20	20	20	18	0.85	5.73				2	0	Inf		996	P
U90915_at	17	0	20	20	20	20	18	0.85	5.47				2	0	Inf		988	P
X16560_at	18	1	20	20	20	20	18	0.90	6.30				4	0	18.0		983	P
X16632_at	16	0	20	20	20	20	18	0.80	5.03				1	0	Inf		971	P
X80909_at	17	0	20	20	20	20	18	0.85	5.63				1	0	Inf		939	P

Side 1

Normal urothelium C										
X15822_at	17	0	20	20	18 0.85	4.56	3	0	Inf	830 P
AF001548_ma1_at	13	1	20	20	18 0.65	3.77	0	0	0 13.0	826 P
U93205_at	15	0	20	20	18 0.75	3.20	0	0	0 Inf	818 P
X13839_at	17	3	20	20	18 0.85	4.84	0	0	0 5.7	801 P
X12447_at	12	1	20	20	18 0.60	2.54	1	1	0 12.0	797 P
Y00503_at	18	0	20	20	18 0.90	4.80	0	0	0 Inf	772 P
X51466_at	16	0	20	20	18 0.80	3.85	0	0	0 Inf	758 P
X68314_at	16	0	20	20	17 0.80	3.82	0	0	0 Inf	739 P
AFFX-HSAC07X00351_5_at	15	1	20	20	18 0.75	3.33	0	0	0 15.0	710 P
AFFX-HUMGAPDH/M33197_M_1	14	2	20	20	18 0.70	2.74	0	0	0 7.0	682 P
X01630_at	13	1	20	20	18 0.65	3.61	0	0	0 13.0	645 P
X62654_ma1_at	16	1	20	20	17 0.80	4.22	0	0	0 16.0	637 P
X67951_at	19	0	20	20	18 0.95	5.08	0	0	0 Inf	608 P
Z84721_cdna2_at	13	3	20	20	18 0.65	3.07	0	0	0 4.3	604 P
U67171_at	14	1	20	20	18 0.70	2.66	0	0	0 14.0	575 P
U84586_at	18	0	20	20	17 0.90	6.10	2	2	0 Inf	559 P
L20688_at	14	0	20	20	17 0.70	3.12	0	0	0 Inf	553 P
X56494_at	12	2	20	20	18 0.60	2.68	1	0	0 6.0	527 P
AFFX-BioDn-5_at	12	1	20	20	18 0.60	3.28	0	1	0 12.0	512 P
X13784_ma1_at	18	1	20	20	18 0.90	5.60	2	2	0 18.0	508 P
X71973_at	14	0	20	20	18 0.70	2.84	0	0	0 Inf	499 P
X82693_at	13	0	20	20	18 0.65	2.55	0	0	0 Inf	492 P
X71874_cdna1_at	15	1	20	20	18 0.75	2.89	0	0	0 15.0	488 P
X55733_at	12	0	20	20	18 0.60	2.95	1	1	0 Inf	487 P
X51521_at	16	1	20	20	18 0.80	4.65	1	0	0 16.0	485 P
X07979_at	16	0	20	20	17 0.80	4.62	0	0	0 Inf	484 P
AFFX-HSAC07X00351_3_at	13	0	20	20	18 0.65	3.47	0	0	0 Inf	449 P
V00572_at	20	0	20	20	18 1.00	5.05	0	0	0 Inf	447 P
Y00282_at	18	0	20	20	18 0.90	4.22	1	0	0 Inf	435 P
U78095_at	13	0	20	20	18 0.65	2.64	0	0	0 Inf	433 P
X02317_at	18	0	20	20	18 0.90	5.43	1	1	0 Inf	428 P
U78294_at	10	2	20	20	18 0.50	1.45	0	0	0 5.0	417 P
U73843_at	13	2	20	20	18 0.65	2.49	0	0	0 6.5	411 P
X80200_at	14	1	20	20	17 0.70	3.92	1	0	0 14.0	409 P
AFFX-HUMGAPDH/M33187_5_e	15	2	20	20	18 0.75	3.89	0	0	0 7.5	404 P
X03100_cdna2_at	11	2	20	20	18 0.55	2.55	0	0	0 5.5	403 P
X77584_at	14	2	20	20	18 0.70	4.06	2	2	1 7.0	400 P
AFFX-BioC-5_at	13	1	20	20	18 0.65	3.47	0	0	0 13.0	397 P
X81817_at	16	2	20	20	18 0.80	3.53	1	1	0 8.0	395 P
Z21507_at	14	2	20	20	18 0.70	3.46	1	0	0 7.0	395 P
V00563_at	14	0	20	20	18 0.70	2.83	0	0	0 Inf	393 P
U77604_at	11	1	20	20	17 0.55	2.46	1	0	0 11.0	374 P
X02152_at	12	3	20	20	18 0.60	2.55	1	0	0 4.0	374 P
X67698_at	17	0	20	20	18 0.85	3.10	0	0	0 Inf	372 P
X14182_at	15	3	20	20	18 0.75	2.37	1	1	1 5.0	370 P
X14727_at	15	1	20	20	18 0.75	4.06	2	0	0 15.0	368 P
X39560_at	11	2	20	20	18 0.55	1.96	0	0	0 5.5	362 P
X75593_at	10	1	20	20	18 0.50	2.70	3	0	0 10.0	359 P
U72511_at	13	0	20	20	18 0.65	2.89	0	0	0 Inf	357 P
X99688_at	11	1	20	20	18 0.55	2.18	0	0	0 11.0	355 P
J02783_at	12	4	20	20	17 0.60	2.08	0	0	0 3.0	351 P
U85611_at	12	1	20	20	18 0.60	3.33	1	1	0 12.0	342 P
X76013_at	15	2	20	20	18 0.75	3.31	1	1	0 7.5	342 P

Normal urothelium C										
X13238_at	15	1	20	20	20	18.075	4.48	0	0.15.0	339 P
X59892_at	11	1	20	20	20	18.055	2.32	0	0.11.0	338 P
Y00764_at	16	1	20	20	20	18.080	4.86	0	0.16.0	335 P
X59417_at	13	0	20	20	20	18.055	3.47	1	0.1nf	327 P
X16135_at	11	3	20	20	20	18.055	2.42	0	0.3.7	326 P
Z48950_at	16	1	20	20	20	18.080	3.45	0	0.16.0	308 P
X75252_at	11	1	20	20	20	18.055	2.58	0	0.11.0	307 P
U90313_at	13	0	20	20	20	18.065	3.28	1	0.1nf	295 P
X88809_at	9	1	20	20	20	18.045	1.66	0	0.9.0	295 P
U78521_at	9	3	20	20	20	18.045	1.36	0	0.3.0	294 P
Z32765_at	12	3	20	20	20	18.080	1.79	0	0.4.0	294 P
Z48199_at	9	0	20	20	20	18.045	2.00	0	0.1nf	294 P
X63331_at	14	0	20	20	20	18.070	3.12	0	0.1nf	293 P
X69908_ma1_at	10	3	20	20	20	18.050	2.47	0	0.3.3	292 P
X75961_at	12	0	20	20	20	18.060	3.38	0	0.1nf	290 P
AFFX-Bloc-3_at	13	2	20	20	20	18.065	2.47	0	0.6.5	287 P
X69111_at	13	3	20	20	20	18.065	2.18	0	0.4.3	284 P
X17042_at	13	0	20	20	20	18.065	4.02	1	0.1nf	280 P
X60221_at	17	2	20	20	20	18.085	3.05	0	0.8.5	278 P
U94569_at	10	2	20	20	20	17.050	1.74	0	0.5.0	270 P
U73824_at	15	0	20	20	20	18.075	3.98	1	0.1nf	268 P
X15880_at	9	2	20	20	20	18.045	2.53	0	0.4.5	267 P
X91257_at	11	0	20	20	20	18.055	2.57	0	0.1nf	266 P
X66253_ma1_at	10	2	20	20	20	18.050	1.39	0	1.5.0	263 P
U94855_at	15	1	20	20	20	17.075	4.00	2	0.15.0	259 P
X91504_at	10	1	20	20	20	17.050	1.34	0	0.10.0	256 P
X67838_at	16	1	20	20	20	17.080	3.65	1	0.16.0	255 P
U86529_at	9	0	20	20	20	18.045	1.84	0	0.1nf	252 P
U72512_at	7	0	20	20	20	17.035	1.27	0	0.1nf	251 P
X74104_at	14	1	20	20	20	18.070	3.37	1	0.14.0	249 P
U66879_at	11	2	20	20	20	18.055	2.30	0	0.5.5	246 P
X04085_ma1_at	11	2	20	20	20	18.055	2.04	0	0.5.5	246 P
X04412_at	9	1	20	20	20	18.045	2.03	0	0.9.0	248 P
Y00281_at	10	0	20	20	20	18.050	2.36	0	0.1nf	244 P
Z27113_at	10	1	20	20	20	18.050	1.98	0	0.10.0	241 P
X78136_at	12	2	20	20	20	18.060	3.45	1	0.6.0	240 P
X66779_at	8	1	20	20	20	18.040	1.38	0	0.8.0	236 P
D13146_cds1_at	10	1	20	20	20	18.050	1.62	0	0.10.0	235 P
X71428_at	12	3	20	20	20	18.060	2.10	1	0.4.0	230 P
U70063_at	11	1	20	20	20	18.055	2.39	0	0.11.0	229 P
U88964_at	12	1	20	20	20	18.060	2.85	0	0.12.0	229 P
U83115_at	12	3	20	20	20	18.060	1.65	0	1.4.0	228 P
X62486_at	12	0	20	20	20	17.060	2.49	0	0.1nf	224 P
X99699_at	9	2	20	20	20	18.045	2.02	0	0.4.5	221 P
U90878_at	13	2	20	20	20	18.065	2.60	0	0.6.5	220 P
X13546_ma1_at	12	1	20	20	20	17.060	2.45	0	0.12.0	216 P
U77948_at	11	1	20	20	20	18.055	2.66	1	0.11.0	215 P
X86693_at	12	2	20	20	20	18.060	3.16	2	0.6.0	212 P
X74801_at	10	1	20	20	20	18.050	2.36	0	0.10.0	211 P
U90199_at	11	1	20	20	20	18.055	2.91	0	0.11.0	209 P
59834_at	13	3	20	20	20	18.065	3.08	1	0.4.3	208 P
5785_ma1_at	8	2	20	20	20	18.040	1.54	0	0.4.0	207 P
89267_at	7	0	20	20	20	18.035	1.18	0	0.1nf	207 P

Sheet 3

Normal urothelium C																			
L10413_at	10	0	20	20	18 0.50	2.06	0	0	0	0	0	0	0	0	0	0	0	0	206 P
U68566_at	9	2	20	20	18 0.45	1.55	0	0	0	0	0	0	0	0	0	0	0	0	203 P
U90716_at	11	2	20	20	18 0.55	3.01	3	3	3	3	3	3	3	3	3	3	3	3	203 P
X83618_at	12	1	20	20	18 0.60	1.90	0	0	0	0	0	0	0	0	0	0	0	0	202 P
X83425_at	9	2	20	20	18 0.45	1.86	0	0	0	0	0	0	0	0	0	0	0	0	201 P
X12794_at	8	1	20	20	18 0.45	1.47	0	0	0	0	0	0	0	0	0	0	0	0	187 P
X60036_at	14	2	20	20	18 0.70	2.41	0	0	0	0	0	0	0	0	0	0	0	0	186 P
X67325_at	10	2	20	20	18 0.50	2.46	0	0	0	0	0	0	0	0	0	0	0	0	194 P
U68142_at	11	1	20	20	18 0.55	2.42	0	0	0	0	0	0	0	0	0	0	0	0	183 P
X52730_rna1_at	8	1	20	20	18 0.40	1.28	0	0	0	0	0	0	0	0	0	0	0	0	182 P
X57346_at	16	0	20	20	17 0.80	3.12	0	0	0	0	0	0	0	0	0	0	0	0	191 P
X74795_at	9	2	20	20	17 0.45	1.61	0	0	0	0	0	0	0	0	0	0	0	0	190 P
X62456_at	13	2	20	20	18 0.65	3.07	0	0	0	0	0	0	0	0	0	0	0	0	190 P
X03218_at	16	0	20	20	17 0.80	3.40	0	0	0	0	0	0	0	0	0	0	0	0	190 P
U79254_at	14	0	20	20	18 0.70	2.90	0	0	0	0	0	0	0	0	0	0	0	0	188 P
X66401_cds1_at	11	2	20	20	18 0.55	3.24	1	1	1	1	1	1	1	1	1	1	1	1	188 P
Z35083_at	10	0	20	20	18 0.50	2.48	0	0	0	0	0	0	0	0	0	0	0	0	188 P
X54304_at	10	0	20	20	18 0.50	2.85	1	1	1	1	1	1	1	1	1	1	1	1	187 P
X70476_at	13	2	20	20	18 0.60	2.55	1	1	1	1	1	1	1	1	1	1	1	1	187 P
X56733_rna1_at	7	1	20	20	18 0.35	3.26	0	0	0	0	0	0	0	0	0	0	0	0	186 P
U68733_rna1_at	11	2	20	20	17 0.55	1.53	0	0	0	0	0	0	0	0	0	0	0	0	185 P
U73379_at	7	1	20	20	18 0.35	1.53	0	0	0	0	0	0	0	0	0	0	0	0	181 P
U77398_at	10	2	20	20	18 0.50	2.09	0	0	0	0	0	0	0	0	0	0	0	0	180 P
X17620_at	7	1	20	20	18 0.35	1.16	0	0	0	0	0	0	0	0	0	0	0	0	178 P
X69910_at	13	2	20	20	18 0.65	2.25	0	0	0	0	0	0	0	0	0	0	0	0	176 P
X98459_at	8	1	20	20	18 0.40	1.40	0	0	0	0	0	0	0	0	0	0	0	0	178 P
X99920_at	12	1	20	20	18 0.60	1.52	0	0	0	0	0	0	0	0	0	0	0	0	176 P
X15414_at	12	0	20	20	17 0.60	2.21	0	0	0	0	0	0	0	0	0	0	0	0	174 P
Z29505_at	15	1	20	20	18 0.75	3.40	1	1	1	1	1	1	1	1	1	1	1	1	174 P
Z37986_at	11	2	20	20	18 0.55	1.92	0	0	0	0	0	0	0	0	0	0	0	0	174 P
Z19574_rna1_at	14	0	20	20	17 0.70	2.84	0	0	0	0	0	0	0	0	0	0	0	0	173 P
U76625_at	7	0	20	20	18 0.35	1.45	0	0	0	0	0	0	0	0	0	0	0	0	172 P
X59434_at	10	2	20	20	18 0.50	1.34	0	0	0	0	0	0	0	0	0	0	0	0	172 P
Y11681_at	9	1	20	20	18 0.45	1.54	0	0	0	0	0	0	0	0	0	0	0	0	172 P
X98209_at	9	2	20	20	18 0.45	1.65	0	0	0	0	0	0	0	0	0	0	0	0	170 P
U72515_at	7	1	20	20	18 0.35	1.29	0	0	0	0	0	0	0	0	0	0	0	0	168 P
U70860_at	11	2	20	20	17 0.55	1.80	0	0	0	0	0	0	0	0	0	0	0	0	160 P
X61970_at	11	2	20	20	18 0.55	2.56	0	0	0	0	0	0	0	0	0	0	0	0	159 P
U94592_at	13	2	20	20	17 0.65	2.02	0	0	0	0	0	0	0	0	0	0	0	0	158 P
X62078_at	12	1	20	20	18 0.60	1.64	0	0	0	0	0	0	0	0	0	0	0	0	157 P
U82010_rna1_at	11	1	20	20	18 0.55	2.44	0	0	0	0	0	0	0	0	0	0	0	0	156 P
X63422_at	10	1	20	20	18 0.50	2.41	0	0	0	0	0	0	0	0	0	0	0	0	156 P
X72964_at	11	1	20	20	18 0.55	1.79	0	0	0	0	0	0	0	0	0	0	0	0	153 P
X76228_at	11	3	20	20	18 0.55	2.46	1	1	1	1	1	1	1	1	1	1	1	1	153 P
U83246_at	8	2	20	20	18 0.40	1.04	0	0	0	0	0	0	0	0	0	0	0	0	152 P
U79296_at	7	1	20	20	18 0.35	1.07	0	0	0	0	0	0	0	0	0	0	0	0	148 P
U90547_at	9	0	20	20	17 0.45	2.01	0	0	0	0	0	0	0	0	0	0	0	0	148 P
X97074_at	6	0	20	20	16 0.40	1.27	0	0	0	0	0	0	0	0	0	0	0	0	146 P
D50405_at	9	1	20	20	18 0.45	1.59	0	0	0	0	0	0	0	0	0	0	0	0	148 P
U93237_rna2_at	10	1	20	20	18 0.50	1.70	0	0	0	0	0	0	0	0	0	0	0	0	146 P
X67237_at	9	1	20	20	18 0.45	1.45	0	0	0	0	0	0	0	0	0	0	0	0	146 P
Z14244_at	13	2	20	20	18 0.65	2.65	1	1	1	1	1	1	1	1	1	1	1	1	146 P
X74295_at	10	1	20	20	18 0.50	1.75	0	0	0	0	0	0	0	0	0	0	0	0	145 P

Normal urothelium C										
X89750_at	14	0	20	20	18.070	3.67	1	0	Inf	145 P
U68233_at	8	2	20	20	18.040	1.71	0	0	0.40	144 P
U72517_at	9	2	20	20	18.045	1.34	0	0	0.45	144 P
X03934_at	10	0	20	20	18.050	2.02	0	0	0 Inf	144 P
U70735_at	12	0	20	20	18.060	1.96	0	0	0 Inf	143 P
U76524_at	10	2	20	20	18.050	1.67	0	0	0.50	143 P
X57398_at	9	1	20	20	18.045	2.09	0	0	0.90	138 P
U87459_at	7	2	20	20	18.035	1.33	0	0	0.35	137 P
X04366_at	10	3	20	20	18.050	2.02	0	0	0.33	137 P
Y00815_at	10	1	20	20	18.050	2.29	0	0	0.10.0	135 P
AFFX-HUMISGF3A/M87835_3_a	10	1	20	20	18.050	1.69	0	0	0.10.0	135 P
U79287_at	8	1	20	20	18.040	1.91	0	0	0.80	135 P
X12451_at	13	0	20	20	17.065	2.96	1	0	0 Inf	135 P
Z49098_at	8	1	20	20	18.040	1.69	1	0	0.80	134 P
X05409_at	11	2	20	20	18.055	1.38	0	0	0.55	133 P
X69433_at	8	2	20	20	18.040	1.33	0	0	0.40	133 P
U75968_at	8	1	20	20	18.040	1.15	0	0	0.80	132 P
L11068_at	9	2	20	20	18.045	1.08	0	0	0.45	132 P
X62744_at	11	3	20	20	17.055	1.93	0	0	0.37	131 P
U89336_cds1_at	8	1	20	20	18.040	1.73	0	0	0.80	130 P
U80907_at	9	2	20	20	18.045	1.38	0	0	0.45	130 P
X82434_at	9	0	20	20	17.045	1.38	0	0	0 Inf	130 P
X82200_at	9	3	20	20	18.045	2.01	1	0	0.30	129 P
X65373_at	10	2	20	20	18.050	1.40	1	0	0.50	129 P
Z47727_at	9	0	20	20	18.045	1.98	0	0	0 Inf	129 P
X71129_at	9	1	20	20	17.045	1.45	0	0	0.90	127 P
U85193_at	10	1	20	20	18.050	2.01	0	0	0.10.0	126 P
X76534_at	14	1	20	20	18.070	3.70	0	0	1.14.0	125 P
Z71460_at	8	2	20	20	18.040	1.42	0	0	0.40	125 P
U81556_at	8	1	20	20	17.040	1.50	0	0	0.80	124 P
U68063_at	10	1	20	20	18.050	3.10	0	0	0.10.0	123 P
X82885_at	7	0	20	20	18.035	1.31	0	0	0 Inf	123 P
X74262_at	14	2	20	20	18.070	3.68	3	0	0.70	120 P
Z56281_at	7	1	20	20	18.035	1.17	0	0	0.70	120 P
X77794_at	16	2	20	20	17.080	3.79	1	0	0.80	119 P
AFFX-Blob3_at	9	0	20	20	18.040	1.05	0	0	0.40	118 P
X54232_at	8	2	20	20	17.045	1.44	0	0	0 Inf	118 P
U78793_at	8	2	20	20	16.040	1.81	0	0	0.40	115 P
X80692_at	10	1	20	20	18.050	2.36	1	0	0.10.0	115 P
X98311_at	9	1	20	20	18.045	1.43	0	0	0.80	113 P
X16316_at	8	2	20	20	18.040	0.98	0	0	0.40	111 P
X04612_at	10	3	20	20	18.050	1.80	0	0	0.33	111 P
X99728_at	11	2	20	20	18.055	1.92	0	0	0.55	110 P
X58405_at	12	1	20	20	18.060	2.86	0	0	0.12.0	109 P
X92886_at	9	3	20	20	17.045	1.52	0	0	0.30	108 P
X76848_at	13	1	20	20	18.085	4.02	1	0	0.13.0	107 P
X15187_at	9	2	20	20	17.045	2.15	0	0	0.45	106 P
U89278_at	8	2	20	20	17.040	0.91	0	0	0.40	105 P
X62055_at	9	1	20	20	17.045	1.53	0	0	0.90	105 P
X68277_at	11	2	20	20	18.055	1.64	0	0	0.55	105 P
X74008_at	11	1	20	20	17.055	2.21	0	0	0.11.0	105 P
U78556_at	9	1	20	20	18.045	1.41	0	0	0.90	104 P
U89336_cds3_at	9	0	20	20	17.045	1.26	0	0	0 Inf	104 P

Slide 5

89
96

X69141_at	12	2	20	20	17.060	2.35	0	0.60	104 P
X78180_at	8	1	20	20	18.040	1.39	0	0.80	104 P
U81932_at	9	1	20	20	17.045	1.82	0	0.90	103 P
Z69720_at	9	2	20	20	17.045	1.15	0	0.45	101 P
U91930_at	11	1	20	20	18.055	2.15	0	0.11.0	100 P
V01512_mna1_at	10	1	20	20	18.050	1.73	0	0.10.0	100 P
Z48042_at	10	2	20	20	18.050	1.74	0	0.50	99 P
X75862_at	8	1	20	20	18.040	1.50	0	0.80	98 P
X84740_at	7	2	20	20	18.035	1.33	0	0.35	98 P
U78241_at	10	3	20	20	17.050	2.01	0	0.33	97 P
X98411_at	8	1	20	20	18.040	1.35	0	0.80	97 P
X79781_at	11	0	20	20	18.055	1.58	0	0.1nf	96 P
U85932_at	7	0	20	20	17.035	1.22	0	0.1nf	95 P
X75304_at	7	0	20	20	18.035	1.21	0	0.1nf	95 P
Z37166_at	10	1	20	20	17.050	1.32	0	0.10.0	94 P
X61123_at	12	1	20	20	17.060	2.74	1	0.12.0	94 P
U80426_at	9	0	20	20	18.045	1.86	1	0.1nf	93 P
X94754_at	9	0	20	20	18.045	1.46	0	0.1nf	93 P
X99585_at	8	2	20	20	18.045	1.19	0	0.45	93 P
X12781_at	9	3	20	20	18.045	1.69	1	0.30	92 P
U86802_at	8	2	20	20	18.040	1.23	0	0.40	91 P
Z47087_at	12	1	20	20	17.060	1.95	0	0.12.0	89 P
U67963_at	7	2	20	20	18.035	1.81	0	0.35	87 P
Z15114_at	10	2	20	20	18.050	1.12	0	0.50	87 P
AFFX-HUMRGE/M10098_5_at	10	1	20	20	17.050	2.34	1	0.10.0	85 P
X57522_at	8	2	20	20	18.040	1.13	1	0.40	85 P
Y08915_at	9	2	20	20	18.045	0.93	0	1.45	85 P
U88629_at	9	2	20	20	17.045	1.88	0	0.45	84 P
X61100_mna1_at	10	0	20	20	18.050	2.11	0	0.1nf	84 P
X91247_at	10	2	20	20	18.050	1.59	0	0.50	84 P
Y07867_at	9	3	20	20	18.045	1.70	0	0.30	84 P
X76538_at	7	2	20	20	18.035	1.88	0	0.35	82 P
X82103_at	10	1	20	20	18.050	1.68	0	0.10.0	82 P
U72514_at	8	2	20	20	18.040	1.89	0	0.40	81 P
X82153_at	13	1	20	20	18.065	2.48	0	0.13.0	81 P
X06614_at	6	2	20	20	18.040	1.41	1	0.40	80 P
Z68747_at	7	2	20	20	18.035	1.32	0	0.35	80 P
U72508_at	7	0	20	20	18.035	1.06	0	0.1nf	79 P
X07024_at	9	2	20	20	18.045	2.76	2	0.45	78 P
Y13115_at	9	2	20	20	18.045	1.27	0	0.45	78 P
U68645_at	7	2	20	20	18.035	1.57	1	0.35	76 P
X63469_at	11	3	20	20	18.055	1.93	0	0.37	75 P
X76057_at	8	1	20	20	18.040	0.98	0	0.80	75 P
Z29083_at	7	1	20	20	17.035	1.39	0	0.70	73 P
X80497_at	8	2	20	20	18.040	1.82	1	0.40	72 P
Z22551_at	9	2	20	20	18.045	1.99	0	0.45	72 P
U77643_at	8	2	20	20	18.040	0.96	0	0.40	71 P
U80919_at	13	3	20	20	18.065	2.64	3	1.43	71 P
X02530_at	7	1	20	20	18.035	1.63	0	0.70	71 P
X05276_at	11	3	20	20	18.055	1.54	1	0.37	71 P
X67155_at	10	3	20	20	18.050	1.51	1	0.33	71 P
U83463_at	11	1	20	20	17.055	2.14	1	0.11.0	69 P
Z70219_at	7	1	20	20	18.035	1.77	0	0.70	69 P

X73079_at	8	2	20	20	17.040	1.14	0	0.40	68 P
Z24725_at	8	1	20	20	18.040	1.83	1	0.80	68 P
Z36531_at	9	3	20	20	18.045	1.96	0	1.30	68 P
Z84709_at	10	1	20	20	18.050	1.50	0	0.10.0	66 P
Z95740_rna2_at	8	2	20	20	18.040	1.27	0	0.40	66 P
Z80910_at	9	2	20	20	18.045	2.08	1	0.45	65 P
U83481_at	8	1	20	20	18.040	1.88	1	0.80	65 P
Y10506_at	9	0	20	20	17.045	2.85	1	0.1nf	65 P
Z35491_at	8	2	20	20	17.040	1.14	0	0.40	64 P
X81003_at	9	0	20	20	18.045	1.85	1	0.1nf	64 P
X04297_at	10	2	20	20	17.050	1.80	1	0.50	63 P
X63753_at	9	1	20	20	17.045	1.90	1	0.90	63 P
U78274_at	11	2	20	20	18.055	2.73	2	0.55	62 P
U96629_rna2_at	8	2	20	20	17.040	1.49	1	0.40	61 P
X83368_at	11	3	20	20	18.055	2.01	2	0.37	60 P
Z50853_at	7	0	20	20	18.035	0.92	0	0.1nf	59 P
AFFX-M27830_5_at	8	2	20	20	18.040	1.43	0	0.40	58 P
X83378_at	9	3	20	20	18.045	1.76	1	0.30	58 P
U79265_at	8	2	20	20	18.040	0.98	0	0.40	57 P
X02612_at	9	3	20	20	18.045	1.57	1	0.30	57 P
X98588_at	11	3	20	20	18.055	2.67	2	0.37	58 P
X98263_at	7	1	20	20	17.035	1.32	1	0.70	58 P
U66469_at	7	1	20	20	18.035	0.92	0	0.70	55 P
X54941_at	8	0	20	20	18.040	1.03	0	0.1nf	55 P
U78313_at	9	1	20	20	17.045	1.42	0	0.90	54 P
U90651_at	9	1	20	20	18.045	1.70	1	1.90	54 P
X65673_at	10	3	20	20	17.050	1.71	0	0.33	52 P
D00960_at	9	2	20	20	18.045	1.05	0	0.45	52 P
X92098_at	8	1	20	20	18.040	1.56	0	0.80	51 P
X68742_at	7	1	20	20	18.035	1.11	0	1.70	48 P
X92396_at	10	1	20	20	18.050	2.18	3	0.10.0	49 P
X59841_at	8	2	20	20	18.040	1.44	0	0.40	48 P
Y12711_at	8	0	20	20	18.055	2.36	2	0.1nf	48 P
X63679_at	8	2	20	20	18.045	1.00	1	1.45	48 P
X85372_at	9	3	20	20	18.045	1.37	0	0.30	47 P
X67212_at	8	2	20	20	18.040	1.84	0	0.40	47 P
X76732_at	8	2	20	20	18.040	1.73	0	0.40	47 P
U78242_at	9	1	20	20	18.045	2.45	2	0.90	46 P
U79273_at	8	2	20	20	17.040	1.90	0	0.40	45 P
X02596_at	8	2	20	20	18.040	1.59	1	0.40	45 P
X53586_rna1_at	8	1	20	20	18.040	1.38	0	1.80	43 P
U86669_at	9	2	20	20	18.045	1.19	0	0.45	40 P
U77129_at	10	2	20	20	18.050	1.39	0	0.50	40 P
X84194_at	9	1	20	20	18.045	2.24	2	0.90	39 P
Z24724_at	8	1	20	20	17.040	1.48	0	0.90	38 P
U73191_at	8	1	20	20	18.045	0.99	0	1.80	37 P
U89338_cds6_at	8	2	20	20	18.045	0.93	0	0.45	35 P
X55544_at	8	1	20	20	18.040	1.33	0	0.80	36 P
X82207_at	7	1	20	20	18.035	1.25	1	0.70	36 P
X66752_at	9	2	20	20	18.045	1.39	1	0.45	36 P
X97544_at	9	0	20	20	18.045	2.38	2	0.1nf	36 P
Y07701_at	8	0	20	20	18.040	1.16	0	0.1nf	36 P

Side 7

Normal urothelium D

Gene name	Pos	Fractl	Log Avg	Pos/Neg	Avg Diff	Abs Call
hum_ali_at	0.93	4.78	19333 P	Under	11710 P	
L04483_s_at	1.00	6.39	8316 P	Under	7387 P	
M63438_s_at	0.94	5.38	7240 P	Under	7095 P	
AFFX-CreX-3_at	1.00	7.08	6543 P	Under	8479 P	
M14199_s_at	1.00	6.11	6165 P	Under	6034 P	
M31520_ma1_s_at	1.00	7.41	5719 P	Under	5581 P	
D13413_ma1_s_at	0.94	5.13	5284 P	Under	5188 P	
J04617_s_at	0.94	6.13	5075 P	Under	4613 P	
J00105_s_at	1.00	8.49	4370 P	Under	4215 P	
HG2815-HT4023_s_at	0.95	5.52	4111 P	Under	4088 P	
AFFX-CreX-5_at	1.00	7.24	3875 P	Under	3716 P	
U06155_s_at	0.86	5.26	3815 P	Under	3097 P	
HG1428-HT1428_s_at	0.90	6.57	3076 P	Under	2957 P	
M10277_s_at	0.90	5.39	2844 P	Under	2759 P	
X52426_s_at	0.95	4.65	2730 P	Under	2639 P	
M25079_s_at	0.75	3.56	2613 P	Under	2532 P	
HG2815-HT2931_at	1.00	4.67	2448 P	Under	2419 P	
X57351_s_at	1.00	6.06	2332 P	Under	2281 P	
AFFX-HSAC07/X00351_3_at	0.95	4.89	2172 P	Under	1884 P	
U43901_ma1_s_at	0.90	4.89	1837 P	Under	1796 P	
M36072_at	0.75	3.70	1747 P	Under	1637 P	
AFFX-HUMGAPDH/M33197_3_a	0.95	5.10	1620 P	Under	1577 P	
V00594_s_at	1.00	6.24	1529 P	Under	1517 P	
X69654_at	0.95	6.24	1510 P	Under	1509 P	
S71043_ma1_s_at	0.80	3.63	1509 P	Under	1509 P	
D48824_s_at	1.00	5.68	1509 P	Under	1509 P	
Z49148_s_at	1.00	5.41	1509 P	Under	1509 P	
X17093_at	0.60	2.80	1509 P	Under	1509 P	
S82297_at	0.95	4.02	1509 P	Under	1509 P	
AFFX-BioDn-3_at	0.75	3.55	1509 P	Under	1509 P	
U68105_s_at	0.95	7.09	1509 P	Under	1509 P	
M34516_at	1.00	3.14	1509 P	Under	1509 P	
M65409_s_at	0.85	5.66	1509 P	Under	1509 P	
X98482_f_at	0.33	1.36	1509 P	Under	1509 P	
X03589_s_at	1.00	0.82	1509 P	Under	1509 P	
HG559-HT658_f_at	0.73	3.32	1509 P	Under	1509 P	
X01677_f_at	0.85	4.02	1509 P	Under	1509 P	
M26708_s_at	1.00	5.58	1509 P	Under	1509 P	
D32128_f_at	0.85	5.02	1509 P	Under	1509 P	
M14483_ma1_s_at	0.80	4.11	1509 P	Under	1509 P	
X51345_at	0.75	4.45	1509 P	Under	1509 P	
HG3991-HT4261_f_at	0.45	2.24	1509 P	Under	1509 P	
M34516_f_at	0.91	4.72	1509 P	Under	1509 P	
X00351_f_at	0.90	5.53	1509 P	Under	1509 P	
D86874_at	0.85	3.82	1509 P	Under	1509 P	
AFFX-HSAC07/X00351_M_at	0.75	3.80	1509 P	Under	1509 P	
HG3342-HT3519_s_at	0.89	5.01	1509 P	Under	1509 P	
M55998_s_at	0.65	5.62	1509 P	Under	1509 P	
HG3431-HT3616_s_at	0.85	6.18	1509 P	Under	1509 P	

Normal urothellum D

HG417-HT417_s_at	0.90	5.16	Under	1481 P
HG2147-HT2217_at	0.83	1.76	5.0	1428 P
M33600_f_at	0.80	3.73	Under	1395 P
X99133_at	0.80	2.86	12.0	1351 P
U57341_f_at	1.00	4.38	Under	1344 P
S54005_s_at	0.80	4.83	Under	1309 P
J04152_ma1_s_at	0.90	5.26	18.0	1281 P
M13560_s_at	0.80	4.20	16.0	1286 P
M24485_s_at	0.65	3.17	Under	1234 P
HG3597-HT3800_f_at	0.80	4.54	16.0	1146 P
M12125_at	0.65	3.02	13.0	1144 P
J03801_f_at	0.90	5.19	Under	1137 P
HG1980-HT2023_at	0.45	2.42	Under	1132 P
M87789_s_at	0.75	2.57	15.0	1078 P
X04347_s_at	0.90	5.03	Under	1076 P
X14008_ma1_f_at	0.75	4.95	15.0	1072 P
S75256_s_at	0.80	3.92	16.0	1089 P
M94880_f_at	0.50	2.24	Under	1061 P
M19311_s_at	0.81	5.08	13.0	1040 P
HG1515-HT1515_f_at	0.75	4.84	15.0	1005 P
AFX-HSAC07X00351_5_at	0.80	3.09	16.0	958 P
J03077_s_at	0.65	3.77	13.0	925 P
X12671_ma1_at	0.90	4.19	Under	917 P
M14328_s_at	0.75	3.54	7.5	885 P
X74929_s_at	0.65	2.81	Under	869 P
L11672_at	0.50	2.21	Under	855 P
U05861_at	0.70	3.82	14.0	850 P
M26730_s_at	0.85	4.45	8.5	838 P
Z19554_s_at	0.78	4.15	14.0	827 P
AFX-HUMGAPDHM33197_M_0.60	0.75	2.75	6.0	802 P
M19045_f_at	0.75	5.50	15.0	794 P
AFX-HSAC07X00351_3_at	0.75	3.50	Under	779 P
HG2815-HT2931_s_at	0.93	4.96	Under	767 P
U70439_s_at	0.75	4.30	Under	766 P
X56681_s_at	0.65	2.68	6.5	766 P
Z48501_s_at	0.74	3.63	Under	748 P
X12876_s_at	0.70	4.75	14.0	745 P
HG3576-HT3779_f_at	0.65	2.88	6.5	734 P
Z89043_s_at	0.70	3.45	7.0	722 P
HG2915-HT3059_f_at	0.65	2.34	Under	720 P
M11313_s_at	0.65	3.19	13.0	717 P
M26311_s_at	0.63	2.85	12.0	686 P
AFX-BioOn-5_at	0.80	3.30	16.0	863 P
HG2917-HT3061_f_at	0.80	2.11	Under	663 P
U04241_at	0.45	2.22	9.0	659 P
D17793_at	0.70	4.00	14.0	650 P
M62403_s_at	0.65	2.40	Under	648 P
HG3236-HT3413_f_at	0.50	2.18	10.0	635 P
L33075_at	0.55	2.57	Under	634 P
X57809_s_at	0.58	2.03	Under	629 P
Z49107_s_at	0.45	1.28	4.5	623 P

Normal urothelium D

AFFX-HUMGAPDHM33187_s_a0.75	4.14	15.0	622 P
U48705_maf_s_at	2.63	3.7	610 P
X03068_f_at	2.29	24.0	606 P
L02326_f_at	2.32	3.7	586 P
AJ000099_s_at	2.08	9.0	546 P
M21142_cd52_s_at	2.18	3.3	546 P
Z15115_at	3.51	Under	543 P
X58841_at	2.13	10.0	540 P
AFFX-BioC-5_at	2.87	6.5	537 P
L06209_s_at	3.77	Under	537 P
HG4264-HT4534_s_at	4.39	Under	530 P
V00598_a_at	2.24	5.5	528 P
X04854_s_at	2.30	4.0	488 P
L40397_at	2.78	14.0	487 P
M96995_s_at	1.58	4.0	470 P
AFFX-BioC-3_at	2.22	6.0	459 P
M83667_maf_s_at	3.14	15.0	444 P
D00749_s_at	1.30	4.5	436 P
U88898_f_at	1.59	Under	422 P
HG1322-HT5143_s_at	3.87	14.0	415 P
U72649_at	2.87	13.0	412 P
U00947_s_at	4.51	Under	403 P
M16336_s_at	2.18	5.5	401 P
X04470_s_at	2.25	Under	398 P
M65292_s_at	2.95	Under	394 P
HG688-HT688_f_at	2.11	12.0	390 P
HG371-HT26388_s_at	2.30	7.0	380 P
M16342_at	2.05	Under	374 P
X58072_at	2.50	Under	373 P
X57351_at	2.13	4.0	369 P
M69013_at	2.79	12.0	368 P
Z26491_s_at	3.48	7.5	361 P
M30448_s_at	2.08	5.5	357 P
L49380_at	1.37	4.5	354 P
U80552_s_at	3.90	Under	347 P
HG3076-HT3238_s_at	2.99	12.0	346 P
X85116_maf_s_at	2.08	3.7	331 P
D17408_s_at	2.31	10.0	325 P
J02871_s_at	2.46	6.0	319 P
M57466_s_at	2.81	Under	312 P
K02405_f_at	1.30	7.0	309 P
M23323_s_at	1.87	11.0	309 P
L3930_s_at	1.68	Under	307 P
X04526_at	2.22	Under	305 P
Z35402_maf_s_at	3.12	14.0	305 P
Y00264_at	3.15	13.0	302 P
L00389_f_at	1.73	Under	301 P
M12659_s_at	2.34	Under	295 P
X15729_s_at	3.92	7.0	295 P
D78577_s_at	2.40	4.0	291 P
M16276_at	1.87	Under	285 P

Normal urothelium D

J05582_s_at	0.50	1.55	Undef	283 P
U08021_at	0.50	1.84	10.0	275 P
M97935_s_at	0.60	2.49	4.0	273 P
D79208_s_at	0.40	1.26	Undef	270 P
X01703_at	0.65	2.81	Undef	267 P
J04093_s_at	0.70	4.37	Undef	265 P
X17567_s_at	0.45	1.85	3.0	261 P
HG4535-HT4940_s_at	0.35	1.29	7.0	259 P
L24774_s_at	0.45	1.63	4.5	259 P
M58525_s_at	0.40	1.38	8.0	259 P
X14684_s_at	0.50	1.79	5.0	258 P
M37457_at	0.50	1.93	Undef	257 P
U49835_s_at	0.60	2.17	Undef	257 P
X94553_xp12_r_at	0.33	1.35	Undef	255 P
M13680_s_at	0.50	2.07	Undef	252 P
S40719_s_at	0.50	1.83	3.3	251 P
X05130_s_at	0.58	1.95	11.0	247 P
U50079_s_at	0.60	2.55	3.0	243 P
AC002045_xp12_s_at	0.55	2.10	11.0	231 P
M10842_at	0.45	2.13	3.0	228 P
D42040_s_at	0.40	1.08	4.0	224 P
L76517_at	0.35	1.27	7.0	221 P
U32988_s_at	0.40	1.48	8.0	218 P
X52979_ma1_s_at	0.55	2.08	11.0	218 P
X53296_s_at	0.65	2.54	5.5	217 P
X90846_at	0.60	1.90	Undef	214 P
AFFX-HUMISGF3AM97935_3_a	0.65	3.14	Undef	209 P
L05187_at	0.45	1.97	9.0	209 P
X65965_s_at	0.67	2.90	Undef	209 P
S50017_s_at	0.55	2.17	5.5	208 P
X72727_at	0.55	1.95	Undef	204 P
X74874_ma1_s_at	0.45	2.13	9.0	203 P
J03805_s_at	0.50	3.17	9.0	202 P
X55037_s_at	0.55	1.49	3.7	201 P
HG4541-HT4946_s_at	0.61	1.85	3.7	197 P
U78528_s_at	0.50	1.17	Undef	195 P
Z49835_s_at	0.50	3.00	5.0	195 P
U03598_at	0.50	1.84	Undef	191 P
L22524_s_at	0.50	2.89	9.0	190 P
M93851_at	0.60	2.33	Undef	190 P
U38341_ma1_at	0.35	1.33	3.5	188 P
M19267_s_at	0.63	2.37	6.0	186 P
U07806_s_at	0.55	2.51	3.7	185 P
M34986_s_at	0.60	2.17	12.0	184 P
X77588_s_at	0.50	1.90	3.3	184 P
L12711_s_at	0.47	1.69	4.5	181 P
S02447_s_at	0.35	1.11	7.0	180 P
U09587_at	0.65	2.63	6.5	178 P
S69272_s_at	0.45	1.49	3.0	177 P
X62083_s_at	0.50	1.18	5.0	177 P
J03242_s_at	0.35	1.56	7.0	172 P

Normal urothellum D

AB006781_s_at	0.35	1.23	Under	171 P
L42583_f_at	0.50	1.38	Under	169 P
X98296_at	0.35	0.98	7.0	169 P
U28014_at	0.60	3.02	Under	169 P
S80437_s_at	0.45	1.55	9.0	166 P
S82597_rna1_s_at	0.50	1.67	10.0	166 P
U16799_s_at	0.60	2.36	4.0	163 P
X57152_rna1_s_at	0.45	1.57	4.5	160 P
X07438_s_at	0.63	3.50	Under	159 P
AFFX-HUMRGE/M10088_s_at	0.55	2.14	5.5	158 P
D00408_s_at	0.45	1.41	Under	156 P
M28213_s_at	0.65	1.93	6.5	156 P
M92843_s_at	0.45	1.62	9.0	154 P
Z11899_s_at	0.40	1.32	4.0	154 P
X73358_s_at	0.47	1.25	4.5	153 P
U77846_rna1_s_at	0.40	1.93	4.0	151 P
X06865_s_at	0.53	2.84	8.0	143 P
M27394_s_at	0.45	1.60	4.5	142 P
U61734_s_at	0.47	1.40	3.0	140 P
Z25521_s_at	0.40	1.23	4.0	140 P
X83416_s_at	0.55	2.60	5.5	139 P
X52022_at	0.45	2.00	Under	138 P
U22431_s_at	0.50	2.19	5.0	135 P
HG2090-HT2152_s_at	0.42	1.54	8.0	132 P
L14778_s_at	0.58	2.72	Under	132 P
D83174_s_at	0.40	1.41	Under	131 P
M13828_s_at	0.45	1.75	3.0	131 P
U41654_at	0.60	1.95	12.0	129 P
U61397_s_at	0.45	1.81	9.0	129 P
M20867_s_at	0.53	2.56	Under	127 P
Y00767_s_at	0.55	2.37	11.0	127 P
Y00451_s_at	0.45	1.77	4.5	125 P
L15189_s_at	0.50	2.51	5.0	124 P
X06700_s_at	0.50	1.59	3.3	124 P
HG2743-HT2846_s_at	0.40	0.91	8.0	123 P
Y00097_s_at	0.50	1.48	3.3	123 P
D83260_s_at	0.47	1.60	4.5	121 P
HG4334-HT4604_s_at	0.35	1.16	7.0	120 P
Z47055_s_at	0.35	1.65	3.5	120 P
X02761_s_at	0.55	1.65	5.5	119 P
X89398_s_at	0.45	0.97	4.5	118 P
D78132_s_at	0.60	1.92	3.0	117 P
D28473_s_at	0.70	2.85	7.0	115 P
S57212_s_at	0.40	1.35	8.0	115 P
HG4657-HT4962_r_at	0.80	1.92	Under	114 P
U61276_s_at	0.50	2.19	10.0	114 P
U60061_at	0.60	2.43	12.0	113 P
J04130_s_at	0.50	1.66	3.3	110 P
M63838_s_at	0.45	2.03	9.0	110 P
S79219_s_at	0.55	1.48	5.5	109 P
U58046_s_at	0.45	2.81	9.0	109 P

297

Normal urothelium D

X03363_s_at	0.35	1.58	3.5	109 P
X76942_s_at	0.60	2.40	6.0	109 P
HG3925-HT14195_at	0.40	1.45	Undef	106 P
M61632_s_at	0.40	1.11	8.0	106 P
U80226_s_at	0.40	1.85	4.0	103 P
X72889_at	0.35	1.53	Undef	103 P
HG3484-HT3678_s_at	0.45	1.66	Undef	99 P
D49372_s_at	0.35	1.28	7.0	97 P
AFFX-M27830_5_at	0.40	1.18	Undef	95 P
S68605_at	0.50	1.96	Undef	94 P
M14745_at	0.50	1.09	10.0	94 P
U06155_at	0.50	1.18	Undef	94 P
Z35086_s_at	0.42	2.60	4.0	93 P
U44799_s_at	0.40	1.60	4.0	92 P
X62534_s_at	0.80	2.49	4.0	92 P
M33684_s_at	0.35	1.42	3.5	91 P
U73936_at	0.45	1.01	Undef	90 P
X85137_s_at	0.40	1.80	8.0	90 P
HG1400-HT1400_s_at	0.50	2.62	10.0	89 P
X80530_at	0.55	2.41	3.7	88 P
X92368_at	0.55	2.41	5.5	87 P
D25535_s_at	0.45	1.84	4.5	87 P
HG4593-HT4998_at	0.50	1.39	3.3	86 P
U41740_at	0.45	2.35	8.0	86 P
X12530_s_at	0.42	1.23	Undef	86 P
AFFX-HUMRGE/M10098_M_at	0.45	1.35	4.5	85 P
U26424_at	0.45	2.48	Undef	84 P
X57809_at	0.50	1.27	4.0	84 P
HG210-HT210_s_at	0.80	2.00	8.0	83 P
HG2981-HT3125_s_at	0.50	1.51	5.0	82 P
U30827_s_at	0.50	1.22	5.0	82 P
M34715_at	0.45	1.39	Undef	80 P
D89377_s_at	0.38	0.97	Undef	78 P
L12760_s_at	0.42	1.78	8.0	75 P
M24069_at	0.45	2.05	3.0	75 P
L43579_s_at	0.40	1.48	3.0	74 P
U01691_s_at	0.35	1.37	Undef	74 P
L00634_s_at	0.53	2.30	3.3	71 P
U19495_s_at	0.65	2.98	4.3	71 P
HG2148-HT2218_f_at	0.35	1.33	3.5	70 P
L25931_s_at	0.55	1.99	11.0	69 P
U20536_s_at	0.45	1.79	Undef	69 P
U77846_ma1_at	0.40	1.34	Undef	68 P
U19147_s_at	0.55	3.75	11.0	66 P
L18677_f_at	0.35	1.26	Undef	64 P
M90356_f_at	0.40	0.92	4.0	63 P
D00003_s_at	0.42	1.46	Undef	62 P
AF012024_s_at	0.40	1.35	4.0	60 P
M16652_at	0.50	1.24	Undef	58 P
U09279_at	0.40	2.24	8.0	58 P
L78933_cds1_at	0.40	1.22	8.0	57 P

Normal urothellum D

M24736_s_at	0.45	2.83	Undef	57 P
D63861_s_at	0.65	3.10	4.3	56 P
U26173_s_at	0.40	0.93	4.0	55 P
U53632_at	0.40	1.11	4.0	53 P
X70944_s_at	0.40	1.97	4.0	53 P
X03350_at	0.45	0.99	9.0	52 P
U20938_at	0.45	1.36	3.0	50 P
X01625_at	0.45	1.93	4.5	48 P
HC38-HT4101_s_at	0.33	1.47	3.0	47 P
U47077_at	0.40	1.22	Undef	47 P
X59244_f_at	0.35	1.32	3.5	47 P
X92493_s_at	0.45	2.05	3.0	47 P
U49020_cd52_s_at	0.35	1.59	3.5	46 P
U72936_s_at	0.35	1.32	7.0	45 P
M14758_at	0.35	1.45	3.5	42 P
S76853_s_at	0.45	1.56	4.5	42 P
M27093_s_at	0.50	1.42	Undef	40 P
M64752_at	0.45	1.07	4.5	38 P
X03490_s_at	0.35	1.38	3.5	38 P
D28235_s_at	0.40	1.37	6.0	37 P
X62429_s_at	0.45	1.66	3.0	36 P
X07235_s_at	0.44	1.44	4.0	35 P
X95632_s_at	0.45	1.86	9.0	35 P
M27436_s_at	0.45	1.65	4.5	32 P
J00219_s_at	0.40	1.18	8.0	31 P
M26665_at	0.50	1.48	3.0	27 P
U09716_s_at	0.35	1.84	3.5	25 P
X01186_s_at	0.35	0.95	7.0	22 P

29

Expressed RNA in Subnormal Connective Tissue, Normal Epithelium and Transitional Carcinomas

Accession	Gene name	Description	Connect. Tite.	Norm. ureth.	Ta. Grl	Ta.Grl	Ta.Grl	Ta.Grl
AB000102	at	Human GABA _A receptor alpha-3 subunit.	351	117	167	170	270	180
AB000111	at	Human mRNA for "olactonodulin", complete cds	194	62	91	37	42	51
AB000115	at	Human "mRNA", complete cds	163	106	44	20	75	92
AB000220	at	Human mRNA for serpinaphorn "E", complete cds	165	78	43	190	28	105
AB000331	at	Human DNA for GPI-anchored molecule, 3aa "protein", complete cds	142	26	37	28	108	26
AB000409	at	Human mRNA for "ANKK1", complete cds	57	70	20	97	235	68
AB000410	at	Human mRNA for "ANKK1", complete cds	20	20	20	20	20	20
AB000410	at	Human mRNA for "ANKK1", complete cds	113	26	67	20	68	20
AB000410	at	Human mRNA for "ANKK1", complete cds	95	85	53	87	20	42
AB000460	at	Human "mRNA", clone "RES4-22B", complete cds	410	209	643	404	658	309
AB000460	at	Human mRNA for "RES4-22B", complete cds	88	108	20	79	213	24
AB000462	at	Human mRNA for B1-3 binding "protein", clone "RES4-23A", complete cds	223	173	199	190	294	256
AB000464	at	Human "mRNA", clone "RES4-24A", exon 1, "2, 3, 4"	20	20	20	20	20	20
AB000465	at	Human "mRNA", clone "RES4-24C", exon 1, "2, 3, 4"	20	20	20	20	20	20
AB000467	at	Human "mRNA", clone "RES4-25", partial cds	134	96	164	138	268	43
AB000468	at	Human mRNA for zinc finger "protein", clone "RES4-26", complete cds	214	286	1029	838	448	249
AB000469	at	Human mRNA for TGF-beta superfamily "protein", complete cds	25	20	20	20	20	20
AB000471	at	Human mRNA for "BMAL1", partial cds, "pB-AB000318 mypse-RNA"	20	20	20	20	20	20
AB000484	at	Human mRNA for "BMAL1", partial cds, "pB-AB000318 mypse-RNA"	20	20	20	20	20	20
AB000485	at	Human mRNA for "BMAL1", partial cds, "pB-AB000318 mypse-RNA"	20	20	20	20	20	20
AB000486	at	Human mRNA for "BMAL1", partial cds, "pB-AB000318 mypse-RNA"	20	20	20	20	20	20
AB000487	at	Human mRNA for "BMAL1", partial cds, "pB-AB000318 mypse-RNA"	20	20	20	20	20	20
AB000488	at	Human mRNA for "BMAL1", partial cds, "pB-AB000318 mypse-RNA"	20	20	20	20	20	20
AB000489	at	Human mRNA for "BMAL1", partial cds, "pB-AB000318 mypse-RNA"	20	20	20	20	20	20
AB000490	at	Human mRNA for "BMAL1", partial cds, "pB-AB000318 mypse-RNA"	20	20	20	20	20	20
AB000491	at	Human mRNA for "BMAL1", partial cds, "pB-AB000318 mypse-RNA"	20	20	20	20	20	20
AB000492	at	Human mRNA for "BMAL1", partial cds, "pB-AB000318 mypse-RNA"	20	20	20	20	20	20
AB000493	at	Human mRNA for "BMAL1", partial cds, "pB-AB000318 mypse-RNA"	20	20	20	20	20	20
AB000494	at	Human mRNA for "BMAL1", partial cds, "pB-AB000318 mypse-RNA"	20	20	20	20	20	20
AB000495	at	Human mRNA for "BMAL1", partial cds, "pB-AB000318 mypse-RNA"	20	20	20	20	20	20
AB000496	at	Human mRNA for "BMAL1", partial cds, "pB-AB000318 mypse-RNA"	20	20	20	20	20	20
AB000497	at	Human mRNA for "BMAL1", partial cds, "pB-AB000318 mypse-RNA"	20	20	20	20	20	20
AB000498	at	Human mRNA for "BMAL1", partial cds, "pB-AB000318 mypse-RNA"	20	20	20	20	20	20
AB000499	at	Human mRNA for "BMAL1", partial cds, "pB-AB000318 mypse-RNA"	20	20	20	20	20	20
AB000500	at	Human mRNA for "BMAL1", partial cds, "pB-AB000318 mypse-RNA"	20	20	20	20	20	20
AB000501	at	Human mRNA for "BMAL1", partial cds, "pB-AB000318 mypse-RNA"	20	20	20	20	20	20
AB000502	at	Human mRNA for "BMAL1", partial cds, "pB-AB000318 mypse-RNA"	20	20	20	20	20	20
AB000503	at	Human mRNA for "BMAL1", partial cds, "pB-AB000318 mypse-RNA"	20	20	20	20	20	20
AB000504	at	Human mRNA for "BMAL1", partial cds, "pB-AB000318 mypse-RNA"	20	20	20	20	20	20
AB000505	at	Human mRNA for "BMAL1", partial cds, "pB-AB000318 mypse-RNA"	20	20	20	20	20	20
AB000506	at	Human mRNA for "BMAL1", partial cds, "pB-AB000318 mypse-RNA"	20	20	20	20	20	20
AB000507	at	Human mRNA for "BMAL1", partial cds, "pB-AB000318 mypse-RNA"	20	20	20	20	20	20
AB000508	at	Human mRNA for "BMAL1", partial cds, "pB-AB0						

[illegible]

[illegible]

Expressed RNA in Endothelial connective tissue, Normal urothelial and Transitional cell carcinomas											
D17408.0.0	Human mRNA for "calpain", complete cds	453	325	20	20	20	20	20	20	20	20
D17427.0	Human mRNA for deaminocyclin type 4	22	37	65	20	20	20	20	20	20	66
D17461.0	Human GULO gene for L-glutono-gulonate oxidase, exon 9, 10' and 12 (p=0.17461) /hyppo-DNA tandem-exon	109	23	74	20	20	20	20	20	20	66
D17516.0	Human mRNA for PACAP "receptor", complete cds	177	95	74	20	20	20	20	20	20	226
D17525.0	Human mRNA for precursor of P100 serine protease of the reactive "factor", complete cds	211	62	81	20	20	20	20	20	20	119
D17532.0	Human mRNA for "RCK", complete cds	20	57	23	20	20	20	20	20	20	41
D17547.0	Human mRNA for DCP/Actinonin isomerase (Nucleoside-related "protein-2"), complete cds	20	20	20	20	20	20	20	20	20	25
D17570.0	Human mRNA for N-acetylglucosaminyltransferase V, complete cds	20	20	20	20	20	20	20	20	20	50
D17716.0	Human mRNA for KIAA0118 "gene", complete cds	232	650	212	20	20	20	20	20	20	50
D17793.0	Human mRNA for KIAA0030 "gene", partial cds	60	20	20	20	20	20	20	20	20	34
D21068.0	Human mRNA for XPC repair complementing protein (p126), complete cds	69	215	226	20	20	20	20	20	20	188
D21069.0	Human mRNA for XPC repair complementing protein (p241/R216), complete cds	51	25	66	20	20	20	20	20	20	82
D21113.0	Human mRNA for KIAA0031 "gene", complete cds	20	20	20	20	20	20	20	20	20	20
D21113.1	Human mRNA for estrogen responsive "type" protein, complete cds	20	43	98	20	20	20	20	20	20	83
D2112.0	Human mRNA for KIAA0032 "gene", complete cds	20	20	20	20	20	20	20	20	20	20
D2112.1	Human mRNA for C3G "protein", complete cds	20	20	20	20	20	20	20	20	20	20
D212.0	Ovary- and prostate-specific exon 1 from Human cytochrome P-450 aromatase "gene", multiple exons 1 and exon 2 (p=0.241) /hyppo-D	77	20	20	20	20	20	20	20	20	41
D212.1	Human mRNA for "C3G" protein, complete cds	20	20	20	20	20	20	20	20	20	20
D212.5	Human mRNA for "C3G" protein, complete cds	20	20	20	20	20	20	20	20	20	20
D2126.0	Human mRNA for KIAA0034 "gene", complete cds	211	123	661	20	20	20	20	20	20	334
D21261.0	Human mRNA for KIAA0120 "gene", complete cds	823	312	788	20	20	20	20	20	20	1786
D21282.0	Human mRNA for KIAA0035 "gene", partial cds	47	20	23	20	20	20	20	20	20	151
D21287.0	Human mRNA for highly expressed protein	78	20	20	20	20	20	20	20	20	20
D21337.0	Human mRNA for collagen	104	58	40	20	20	20	20	20	20	66
D21861.0	Human mRNA for KIAA0028 "gene", partial cds	104	86	178	20	20	20	20	20	20	66
D21862.0	Human mRNA for KIAA0029 "gene", partial cds	20	20	72	20	20	20	20	20	20	77
D21863.0	Human mRNA for "B3T-1", complete cds	108	90	267	20	20	20	20	20	20	194
D21876.0	Human mRNA for ribosomal "protein", complete cds	6346	4257	5768	20	20	20	20	20	20	2421
D23682.0	Human mRNA for ubiquitin-like "protein", complete cds	417	486	567	20	20	20	20	20	20	400
D23675.0	Human "RNA", clone H1103 (derived by the monoclonal antibody of insulin receptor subunit-1 (IR-3-1))	312	401	620	20	20	20	20	20	20	448
D25216.0	Human mRNA for KIAA0032 "gene", complete cds	34	22	24	20	20	20	20	20	20	21
D25216.1	Human mRNA for KIAA0014 "gene", complete cds	127	265	581	20	20	20	20	20	20	532
D25217.0	Human mRNA for KIAA0037 "gene", partial cds	139	70	117	20	20	20	20	20	20	20
D25218.0	Human mRNA for KIAA0112 "gene", partial cds	300	43	182	20	20	20	20	20	20	20
D25248.0	Human randomly sequenced mRNA	124	57	98	20	20	20	20	20	20	20
D25274.0	Human randomly sequenced mRNA	378	342	588	20	20	20	20	20	20	294
D25276.0	Human mRNA for KIAA0038 "gene", complete cds	87	88	60	20	20	20	20	20	20	119
D25303.0	Human mRNA for integrin alpha "subunit", complete cds	89	52	20	20	20	20	20	20	20	167
D25304.0	Human mRNA for KIAA0006 "gene", partial cds	30	20	20	20	20	20	20	20	20	108
D25320.0	Human mRNA for placenta-type "prothrombinase", complete cds	37	20	20	20	20	20	20	20	20	20
D25330.0	Human mRNA for KIAA0037 "gene", complete cds	20	20	20	20	20	20	20	20	20	20
D25336.0	Human mRNA for KIAA0040 "gene", complete cds	26	20	20	20	20	20	20	20	20	20
D25341.0	Human mRNA for PIAT "autophagy", complete cds	54	20	20	20	20	20	20	20	20	20
D26016.0	Human mRNA for KIAA0039 "gene", partial cds	45	20	20	20	20	20	20	20	20	20
D26047.0	Human mRNA for KIAA0038 "gene", partial cds	20	20	20	20	20	20	20	20	20	20
D26068.0	Human mRNA for KIAA0041 "gene", partial cds	821	323	654	20	20	20	20	20	20	408
D26069.0	Human mRNA for type 1 "protein", 1,4,5-triphosphate "receptor", complete cds	20	20	248	20	20	20	20	20	20	41
D26070.0	Human mRNA for ribonuclease A (RNase A), complete cds	47	25	21	20	20	20	20	20	20	20
D26135.0	Human mRNA for diacylglycerol kinase "protein", complete cds	237	128	20	20	20	20	20	20	20	1524
D26155.0	Human mRNA for transglutaminase "protein", complete cds	20	20	20	20	20	20	20	20	20	20
D26156.0	Human mRNA for transglutaminase "protein", complete cds	86	36	288	20	20	20	20	20	20	228
D26308.0	Human mRNA for KIAA0042 "gene", complete cds	554	270	32	20	20	20	20	20	20	255
D26350.0	Human mRNA for type 2 "protein", 1,4,5-triphosphate "receptor", complete cds	20	20	20	20	20	20	20	20	20	20
D26351.0	Human mRNA for KIAA0043 "gene", partial cds	20	20	20	20	20	20	20	20	20	71
D26382.0	Human mRNA for KIAA0044 "gene", complete cds	20	20	20	20	20	20	20	20	20	121
D26443.0	Human mRNA for KIAA0045 "gene", complete cds	20	20	20	20	20	20	20	20	20	38
D26520.0	Human gene for cytochrome P-450 "aromatase", complete cds (exon 1-15)	108	20	20	20	20	20	20	20	20	43
D26535.0	Human papillomavirus B6 genome integrated into human carcinoma DNA	43	97	252	20	20	20	20	20	20	25
D26561.0	Human papillomavirus B6 genome integrated into human carcinoma DNA	63	47	75	20	20	20	20	20	20	20
D26561.0	Human papillomavirus B6 genome integrated into human carcinoma DNA	20	33	20	20	20	20	20	20	20	20
D26578.0	Human mRNA for transmembrane "protein", complete cds	66	89	20	20	20	20	20	20	20	209
D26598.0	Human mRNA for proteasome subunit "Hsc70-1", complete cds	359	394	440	20	20	20	20	20	20	512
D26599.0	Human mRNA for proteasome subunit "Hsc70-1", complete cds	387	269	352	20	20	20	20	20	20	557
D28000.0	Human mRNA for proteasome subunit "Hsc70-1", complete cds	70	218	251	20	20	20	20	20	20	261

Expressed RNA in Subcutaneous connective tissue, Normal urothelium and Transitional cell carcinoma									
Accession	Gene	Transcript	Length	GC	GC	GC	GC	GC	GC
D20114.at	Human mRNA for MOBP (myelin-associated oligodendrocyte basic protein), complete cds		58	136	46	135	46	135	161
D20116.at	Human mRNA for "D81", complete cds		27	40	66	70	66	70	20
D20124.at	Human mRNA for unknown product, complete cds		552	314	348	466	348	466	442
D20137.at	Human mRNA for "B17-2", complete cds		176	94	198	168	198	168	195
D20235.at	Human P1322 gene for proteinase 2, complete cds		47	37	65	20	65	20	33
D20294.at	Human mRNA for ATP synthase B chain, 5'UTR (sequence from the 5' cap to the start codon), /gp=D20364 mypse-rna		208	83	46	128	46	128	47
D20293.at	Human mRNA for ATP synthase B chain, 5'UTR (sequence from the 5' cap to the start codon), /gp=D20363 mypse-rna		219	87	218	728	218	728	343
D20416.at	Human mRNA for proteinase 2, 5'UTR (sequence from the 5' cap to the start codon), /gp=D20416 mypse-rna		301	182	223	364	223	364	185
D20423.at	Human T lymphocyte mRNA for islet-1, complete cds		241	91	280	258	280	258	312
D20473.at	Human T lymphocyte mRNA for islet-1, complete cds		68	115	257	104	257	104	139
D20476.at	Human mRNA for KIAA0045 gene, complete cds		76	68	204	45	204	45	20
D20483.at	Human mRNA for KIAA0045 gene, complete cds		87	73	215	76	215	76	134
D20532.at	Human mRNA for KIAA0045 gene, complete cds		89	73	31	40	31	40	68
D20538.at	Human mRNA for KIAA0045 gene, complete cds		20	20	20	20	20	20	20
D20548.at	Human mRNA for KIAA0045 gene, complete cds		39	34	160	20	160	20	41
D20589.at	Human P163 gene, 5' flanking region and		20	20	104	20	104	20	38
D20613.at	Human gene for human C-associated microtubule associated protein p44		93	125	28	41	28	41	164
D20612.at	Human mRNA for KIAA0051 gene, complete cds		71	63	44	403	44	403	954
D20613.at	Human mRNA for KIAA0051 gene, complete cds		48	32	227	140	227	140	171
D20613.at	Human mRNA for KIAA0051 gene, complete cds		98	77	42	51	42	51	41
D20613.at	Human mRNA for KIAA0051 gene, complete cds		78	36	20	30	20	30	79
D20613.at	Human mRNA for KIAA0051 gene, complete cds		221	120	273	237	273	237	72
D20613.at	Human mRNA for KIAA0051 gene, complete cds		65	93	75	121	75	121	51
D20613.at	Human mRNA for KIAA0051 gene, complete cds		20	20	20	20	20	20	20
D20613.at	Human mRNA for KIAA0051 gene, complete cds		291	77	171	118	171	118	82
D20613.at	Human mRNA for KIAA0051 gene, complete cds		20	20	20	20	20	20	53
D20613.at	Human mRNA for KIAA0051 gene, complete cds		169	120	209	218	209	218	87
D20613.at	Human mRNA for KIAA0051 gene, complete cds		20	20	20	20	20	20	387
D20613.at	Human mRNA for KIAA0051 gene, complete cds		43	39	74	44	74	44	45
D20613.at	Human mRNA for KIAA0051 gene, complete cds		277	482	443	475	443	475	331
D20613.at	Human mRNA for KIAA0051 gene, complete cds		20	20	20	20	20	20	20
D20613.at	Human mRNA for KIAA0051 gene, complete cds		85	41	48	44	48	44	105
D20613.at	Human mRNA for KIAA0051 gene, complete cds		391	728	949	878	949	878	814
D20613.at	Human mRNA for KIAA0051 gene, complete cds		20	65	27	76	27	76	125
D20613.at	Human mRNA for KIAA0051 gene, complete cds		20	20	20	20	20	20	20
D20613.at	Human mRNA for KIAA0051 gene, complete cds		68	116	20	76	20	76	127
D20613.at	Human mRNA for KIAA0051 gene, complete cds		100	64	109	103	109	103	107
D20613.at	Human mRNA for KIAA0051 gene, complete cds		136	188	81	124	81	124	211
D20613.at	Human mRNA for KIAA0051 gene, complete cds		25	20	72	21	72	21	140
D20613.at	Human mRNA for KIAA0051 gene, complete cds		20	33	45	22	45	22	77
D20613.at	Human mRNA for KIAA0051 gene, complete cds		48	35	98	34	98	34	78
D20613.at	Human mRNA for KIAA0051 gene, complete cds		117	72	233	210	233	210	301
D20613.at	Human mRNA for KIAA0051 gene, complete cds		238	85	182	167	182	167	204
D20613.at	Human mRNA for KIAA0051 gene, complete cds		236	205	620	395	620	395	204
D20613.at	Human mRNA for KIAA0051 gene, complete cds		44	20	20	20	20	20	20
D20613.at	Human mRNA for KIAA0051 gene, complete cds		44	48	35	20	48	35	46
D20613.at	Human mRNA for KIAA0051 gene, complete cds		20	20	20	20	20	20	20
D20613.at	Human mRNA for KIAA0051 gene, complete cds		20	20	20	20	20	20	20
D20613.at	Human mRNA for KIAA0051 gene, complete cds		20	20	20	20	20	20	20
D20613.at	Human mRNA for KIAA0051 gene, complete cds		402	424	353	370	424	353	584
D20613.at	Human mRNA for KIAA0051 gene, complete cds		567	431	341	210	431	341	20
D20613.at	Human mRNA for KIAA0051 gene, complete cds		205	103	143	182	143	182	267
D20613.at	Human mRNA for KIAA0051 gene, complete cds		76	103	393	205	393	205	182
D20613.at	Human mRNA for KIAA0051 gene, complete cds		20	20	20	20	20	20	20
D20613.at	Human mRNA for KIAA0051 gene, complete cds		63	20	100	20	100	20	20
D20613.at	Human mRNA for KIAA0051 gene, complete cds		33	20	32	20	32	20	20
D20613.at	Human mRNA for KIAA0051 gene, complete cds		135	160	297	218	297	218	188
D20613.at	Human mRNA for KIAA0051 gene, complete cds		98	64	79	145	79	145	308
D20613.at	Human mRNA for KIAA0051 gene, complete cds		141	25	125	125	125	125	168

[illegible]

[illegible]

[illegible]

Expressed RNA in Subendothelial connective tissue, Normal endothelium and Transendothelial cell carcinoma

Accession	Gene	48	23	64	49	44	40
D86550.at	Human mRNA for perlecanin protein "Kinaso", complete cds	20	20	20	20	20	20
D86640.at	Human mRNA for "sluc", complete cds	52	63	69	90	69	52
D86956.at	Human mRNA for KIAA0201 "gene", partial cds	25	106	45	43	20	65
D86957.at	Human mRNA for KIAA0202 "gene", complete cds	20	20	20	20	20	20
D86958.at	Human mRNA for KIAA0203 "gene", complete cds	20	20	20	20	20	20
D86959.at	Human mRNA for KIAA0204 "gene", complete cds	60	38	102	58	20	42
D86960.at	Human mRNA for KIAA0205 "gene", complete cds	31	41	35	37	23	67
D86961.at	Human mRNA for KIAA0206 "gene", partial cds	31	41	20	35	20	20
D86962.at	Human mRNA for KIAA0207 "gene", complete cds	74	91	171	81	151	55
D86963.at	Human mRNA for KIAA0208 "gene", complete cds	128	20	154	88	20	85
D86964.at	Human mRNA for KIAA0209 "gene", partial cds	33	20	20	20	20	20
D86965.at	Human mRNA for KIAA0210 "gene", complete cds	155	215	98	148	199	361
D86966.at	Human mRNA for KIAA0211 "gene", complete cds	188	60	82	135	255	185
D86967.at	Human mRNA for KIAA0212 "gene", partial cds	73	41	64	104	319	138
D86968.at	Human mRNA for KIAA0213 "gene", complete cds	20	20	20	20	20	20
D86969.at	Human mRNA for KIAA0214 "gene", complete cds	32	41	20	20	48	20
D86970.at	Human mRNA for KIAA0215 "gene", complete cds	77	77	20	20	22	20
D86971.at	Human mRNA for KIAA0216 "gene", complete cds	45	20	45	20	20	49
D86972.at	Human mRNA for KIAA0217 "gene", partial cds	116	138	45	73	427	144
D86973.at	Human mRNA for KIAA0218 "gene", complete cds	519	1677	4011	2341	4881	4376
D86974.at	Human mRNA for KIAA0219 "gene", partial cds	91	76	20	20	20	20
D86975.at	Human mRNA for KIAA0220 "gene", complete cds	20	124	53	90	28	108
D86976.at	Human mRNA for KIAA0221 "gene", partial cds	69	131	88	85	119	108
D86977.at	Human mRNA for KIAA0222 "gene", complete cds	39	114	20	20	78	139
D86978.at	Human mRNA for KIAA0223 "gene", partial cds	20	20	20	20	48	31
D86979.at	Human mRNA for KIAA0224 "gene", complete cds	34	20	38	39	187	20
D86980.at	Human mRNA for KIAA0225 "gene", complete cds	52	77	121	64	180	132
D86981.at	Human mRNA for KIAA0226 "gene", partial cds	89	42	98	32	59	103
D86982.at	Human mRNA for KIAA0227 "gene", complete cds	20	20	20	20	162	20
D86983.at	Human mRNA for KIAA0228 "gene", partial cds	43	58	53	73	20	38
D86984.at	Human mRNA for KIAA0229 "gene", complete cds	151	130	218	178	405	281
D86985.at	Human (lambda) DNA for immunoglobulin light chain	20	20	20	20	20	20
D86986.at	Human (lambda) DNA for immunoglobulin light chain	20	20	20	20	20	20
D86987.at	Human (lambda) DNA for immunoglobulin light chain	23	20	20	20	20	20
D86988.at	Human (lambda) DNA for immunoglobulin light chain	223	270	369	344	176	68
D86989.at	Human (lambda) DNA for immunoglobulin light chain	64	20	20	20	20	20
D86990.at	Human (lambda) DNA for immunoglobulin light chain	157	123	20	20	20	197
D86991.at	Human (lambda) DNA for immunoglobulin light chain	24	39	27	20	20	20
D86992.at	Human mRNA for KIAA0223 "gene", complete cds	20	20	20	20	108	20
D86993.at	Human mRNA for KIAA0224 "gene", complete cds	26	20	71	54	246	204
D86994.at	Human mRNA for KIAA0225 "gene", partial cds	28	59	20	20	20	20
D86995.at	Human mRNA for KIAA0226 "gene", partial cds	28	20	20	20	20	20
D86996.at	Human mRNA for KIAA0227 "gene", partial cds	46	20	58	28	20	64
D86997.at	Human mRNA for KIAA0228 "gene", complete cds	91	66	20	20	20	32
D86998.at	Human mRNA for KIAA0229 "gene", complete cds	43	85	20	20	49	32
D86999.at	Human cDNA for KIAA0230 "gene", complete cds	20	20	37	53	20	20
D87000.at	Human cDNA for KIAA0231 "gene", complete cds	20	20	431	63	20	20
D87001.at	Human cDNA for KIAA0232 "gene", complete cds	20	20	20	20	20	20
D87002.at	Human cDNA for KIAA0233 "gene", complete cds	20	20	20	20	20	20
D87003.at	Human cDNA for KIAA0234 "gene", complete cds	20	20	20	20	20	20
D87004.at	Human cDNA for KIAA0235 "gene", complete cds	20	20	20	20	20	20
D87005.at	Human cDNA for KIAA0236 "gene", complete cds	20	20	20	20	20	20
D87006.at	Human cDNA for KIAA0237 "gene", complete cds	20	20	20	20	20	20
D87007.at	Human cDNA for KIAA0238 "gene", complete cds	20	20	20	20	20	20
D87008.at	Human cDNA for KIAA0239 "gene", complete cds	20	20	20	20	20	20
D87009.at	Human cDNA for KIAA0240 "gene", complete cds	20	20	20	20	20	20
D87010.at	Human cDNA for KIAA0241 "gene", complete cds	20	20	20	20	20	20
D87011.at	Human cDNA for KIAA0242 "gene", complete cds	20	20	20	20	20	20
D87012.at	Human cDNA for KIAA0243 "gene", complete cds	20	20	20	20	20	20
D87013.at	Human cDNA for KIAA0244 "gene", complete cds	20	20	20	20	20	20
D87014.at	Human cDNA for KIAA0245 "gene", complete cds	20	20	20	20	20	20
D87015.at	Human cDNA for KIAA0246 "gene", complete cds	20	20	20	20	20	20
D87016.at	Human cDNA for KIAA0247 "gene", complete cds	20	20	20	20	20	20
D87017.at	Human cDNA for KIAA0248 "gene", complete cds	20	20	20	20	20	20
D87018.at	Human cDNA for KIAA0249 "gene", complete cds	20	20	20	20	20	20
D87019.at	Human cDNA for KIAA0250 "gene", complete cds	20	20	20	20	20	20
D87020.at	Human cDNA for KIAA0251 "gene", complete cds	20	20	20	20	20	20
D87021.at	Human cDNA for KIAA0252 "gene", complete cds	20	20	20	20	20	20
D87022.at	Human cDNA for KIAA0253 "gene", complete cds	20	20	20	20	20	20
D87023.at	Human cDNA for KIAA0254 "gene", complete cds	20	20	20	20	20	20
D87024.at	Human cDNA for KIAA0255 "gene", complete cds	20	20	20	20	20	20
D87025.at	Human cDNA for KIAA0256 "gene", complete cds	20	20	20	20	20	20
D87026.at	Human cDNA for KIAA0257 "gene", complete cds	20	20	20	20	20	20
D87027.at	Human cDNA for KIAA0258 "gene", complete cds	20	20	20	20	20	20
D87028.at	Human cDNA for KIAA0259 "gene", complete cds	20	20	20	20	20	20
D87029.at	Human cDNA for KIAA0260 "gene", complete cds	20	20	20	20	20	20
D87030.at	Human cDNA for KIAA0261 "gene", complete cds	20	20	20	20	20	20
D87031.at	Human cDNA for KIAA0262 "gene", complete cds	20	20	20	20	20	20
D87032.at	Human cDNA for KIAA0263 "gene", complete cds	20	20	20	20	20	20
D87033.at	Human cDNA for KIAA0264 "gene", complete cds	20	20	20	20	20	20
D87034.at	Human cDNA for KIAA0265 "gene", complete cds	20	20	20	20	20	20
D87035.at	Human cDNA for KIAA0266 "gene", complete cds	20	20	20	20	20	20
D87036.at	Human cDNA for KIAA0267 "gene", complete cds	20	20	20	20	20	20
D87037.at	Human cDNA for KIAA0268 "gene", complete cds	20	20	20	20	20	20
D87038.at	Human cDNA for KIAA0269 "gene", complete cds	20	20	20	20	20	20
D87039.at	Human cDNA for KIAA0270 "gene", complete cds	20	20	20	20	20	20
D87040.at	Human cDNA for KIAA0271 "gene", complete cds	20	20	20	20	20	20
D87041.at	Human cDNA for KIAA0272 "gene", complete cds	20	20	20	20	20	20
D87042.at	Human cDNA for KIAA0273 "gene", complete cds	20	20	20	20	20	20
D87043.at	Human cDNA for KIAA0274 "gene", complete cds	20	20	20	20	20	20
D87044.at	Human cDNA for KIAA0275 "gene", complete cds	20	20	20	20	20	20
D87045.at	Human cDNA for KIAA0276 "gene", complete cds	20	20	20	20	20	20
D87046.at	Human cDNA for KIAA0277 "gene", complete cds	20	20	20	20	20	20

Human pyruvate dehydrogenase (EC 1.2.4.1) beta subunit "Homo", isoform 1 (HLM)	125	102	147	20	130
Human AMY2B gene for alpha-amylase	20	209	329	20	246
Human mRNA for DNA binding protein TAXREB07	380	209	44	20	240
Human mRNA for glycoprotein 34 (gp34)	20	132	268	20	158
Human CSAT gene for non-specific cross-reacting antigen (NSCA)	148	20	20	20	100
Human mRNA for collagen alpha 1(V) chain, complete cds	20	20	20	20	20
Human carboxyl phosphate synthetase I (EC 6.3.4.10) mRNA	54	20	20	20	20
Human CCG1 mRNA	20	20	20	20	20
Human CCG1.1	20	20	20	20	20
Human CCG1.2	20	20	20	20	20
Human CCG1.3	20	20	20	20	20
Human CCG1.4	20	20	20	20	20
Human CCG1.5	20	20	20	20	20
Human CCG1.6	20	20	20	20	20
Human CCG1.7	20	20	20	20	20
Human CCG1.8	20	20	20	20	20
Human CCG1.9	20	20	20	20	20
Human CCG1.10	20	20	20	20	20
Human CCG1.11	20	20	20	20	20
Human CCG1.12	20	20	20	20	20
Human CCG1.13	20	20	20	20	20
Human CCG1.14	20	20	20	20	20
Human CCG1.15	20	20	20	20	20
Human CCG1.16	20	20	20	20	20
Human CCG1.17	20	20	20	20	20
Human CCG1.18	20	20	20	20	20
Human CCG1.19	20	20	20	20	20
Human CCG1.20	20	20	20	20	20
Human CCG1.21	20	20	20	20	20
Human CCG1.22	20	20	20	20	20
Human CCG1.23	20	20	20	20	20
Human CCG1.24	20	20	20	20	20
Human CCG1.25	20	20	20	20	20
Human CCG1.26	20	20	20	20	20
Human CCG1.27	20	20	20	20	20
Human CCG1.28	20	20	20	20	20
Human CCG1.29	20	20	20	20	20
Human CCG1.30	20	20	20	20	20
Human CCG1.31	20	20	20	20	20
Human CCG1.32	20	20	20	20	20
Human CCG1.33	20	20	20	20	20
Human CCG1.34	20	20	20	20	20
Human CCG1.35	20	20	20	20	20
Human CCG1.36	20	20	20	20	20
Human CCG1.37	20	20	20	20	20
Human CCG1.38	20	20	20	20	20
Human CCG1.39	20	20	20	20	20
Human CCG1.40	20	20	20	20	20
Human CCG1.41	20	20	20	20	20
Human CCG1.42	20	20	20	20	20
Human CCG1.43	20	20	20	20	20
Human CCG1.44	20	20	20	20	20
Human CCG1.45	20	20	20	20	20
Human CCG1.46	20	20	20	20	20
Human CCG1.47	20	20	20	20	20
Human CCG1.48	20	20	20	20	20
Human CCG1.49	20	20	20	20	20
Human CCG1.50	20	20	20	20	20
Human CCG1.51	20	20	20	20	20
Human CCG1.52	20	20	20	20	20
Human CCG1.53	20	20	20	20	20
Human CCG1.54	20	20	20	20	20
Human CCG1.55	20	20	20	20	20
Human CCG1.56	20	20	20	20	20
Human CCG1.57	20	20	20	20	20
Human CCG1.58	20	20	20	20	20
Human CCG1.59	20	20	20	20	20

[illegible]

[illegible]

Expressed RNA in Subepithelial connective tissue, Normal epithelium and Transitional cell carcinoma									
HG3405-HT3585, at	Zinc Finger Protein 123 (Gp300/153)	72	20	20	20	20	20	20	20
HG3412-HT3583, at	Blue Cone Photoreceptor Pigment	20	20	20	20	20	20	20	20
HG3415-HT3580, at	Polevivirus Receptor	120	20	20	20	20	20	20	20
HG3417-HT3580, at	Glycylglycylase 1, Alt. Splice 1	43	67	67	67	67	67	67	67
HG3428-HT3610, at	Zinc Finger Protein 1, Alt. Splice 1	1128	1529	1529	1529	1529	1529	1529	1529
HG3431-HT3616, at	"Decorin", Alt. Splice 1	95	28	28	28	28	28	28	28
HG3432-HT3616, at	Fibroblast Growth Factor Receptor "K-Sam", Alt. Splice 1	20	20	20	20	20	20	20	20
HG3433-HT3620, at	Fibroblast Growth Factor Receptor "K-Sam", Alt. Splice 3, K-Sam III	20	20	20	20	20	20	20	20
HG3434-HT3620, at	Fibroblast Growth Factor Receptor "K-Sam", Alt. Splice 4, K-Sam IV	20	20	20	20	20	20	20	20
HG3437-HT3628, at	Myosin (Prodomain) Protein, Alt. Splice 2	54	47	47	47	47	47	47	47
HG3444-HT3647, at	Zinc Finger Protein 22	20	20	20	20	20	20	20	20
HG3477-HT3670, at	Cd4 Antigen	63	66	66	66	66	66	66	66
HG3484-HT3678, at	Protein Kinase (Gp-M50287)	20	20	20	20	20	20	20	20
HG3481-HT3695, at	Zinc Finger Protein Zip-36	43	135	135	135	135	135	135	135
HG3482-HT3686, at	Uncoupling Protein Ucp	416	217	217	217	217	217	217	217
HG3484-HT3688, at	Nuclear Factor NF-115	22	20	20	20	20	20	20	20
HG3485-HT3688, at	Collagen, Type "I", Alpha 1	48	103	103	103	103	103	103	103
HG3486-HT3688, at	Homeotic Protein Hox5.4	20	20	20	20	20	20	20	20
HG3487-HT3688, at	V-ErbA Related E2F-3 Protein	20	20	20	20	20	20	20	20
HG3488-HT3688, at	"Myosin", Heavy, Polypeptide 5, Light Meromyosin	189	191	191	191	191	191	191	191
HG3489-HT3688, at	Tropomyosin (Troponin) Cysteine	164	164	164	164	164	164	164	164
HG3490-HT3688, at	Alpha-1 Antitrypsin, S End	122	122	122	122	122	122	122	122
HG3491-HT3688, at	Protein-Organic C-Myc, Alt. Splice 3, C-Myc 114	51	51	51	51	51	51	51	51
HG3492-HT3688, at	Leukocyte Homophilic, Beta Subunit	150	143	143	143	143	143	143	143
HG3493-HT3688, at	Insulin-Like Growth Factor 2	30	30	30	30	30	30	30	30
HG3494-HT3688, at	Pre-MRNA Splicing Factor "Srp33", Alt. Splice Form 1	39	39	39	39	39	39	39	39
HG3495-HT3688, at	Coat Displacement Protein, Cyt. Hemoglobin, Alt. Splice 1	3943	4127	4127	4127	4127	4127	4127	4127
HG3496-HT3688, at	Wnt5b Tumor-Related Protein	20	20	20	20	20	20	20	20
HG3497-HT3688, at	Zinc Finger Protein (Gp-M8357)	48	39	39	39	39	39	39	39
HG3498-HT3688, at	Zinc Finger Protein (Gp-M8357)	14	110	110	110	110	110	110	110
HG3499-HT3688, at	Zinc Finger Protein (Gp-M8357)	144	28	28	28	28	28	28	28
HG3500-HT3688, at	Protein Phosphatase Inhibitor Homolog	385	734	734	734	734	734	734	734
HG3501-HT3688, at	Major Histocompatibility Complex, Class II Beta W52	54	77	77	77	77	77	77	77
HG3502-HT3688, at	Autocrine "Antigen", Thyroid Disease-Related Antigen	153	178	178	178	178	178	178	178
HG3503-HT3688, at	Homeotic Protein 7, Nidh Group	422	1149	1149	1149	1149	1149	1149	1149
HG3504-HT3688, at	Major Histocompatibility Complex, Class I (Gp-X12432)	24	47	47	47	47	47	47	47
HG3505-HT3688, at	Calcium Channel, "Voltage-Gated", Beta 1 "Subunit", Alt. Splice 2, Skeletal Muscle Isoform	83	74	74	74	74	74	74	74
HG3506-HT3688, at	Epidermal Growth Factor Receptor-Related Protein	20	20	20	20	20	20	20	20
HG3507-HT3688, at	Zinc Finger Protein, Kuppfer-Like	20	20	20	20	20	20	20	20
HG3508-HT3688, at	"Myosin", Heavy Polypeptide 5, Non-Muscle	60	60	60	60	60	60	60	60
HG3509-HT3688, at	Amphid Beta (A4) Precursor Protein, Alt. Splice 2, A4(75)	77	87	87	87	87	87	87	87
HG3510-HT3688, at	Amphid Beta (A4) Precursor Protein, Alt. Splice 4	20	20	20	20	20	20	20	20
HG3511-HT3688, at	Utp-Glucuronosyltransferase 1, Family, Polypeptide 1, Alt. Splice 1	20	20	20	20	20	20	20	20
HG3512-HT3688, at	Guanine Nucleotide-Binding Protein, Alpha Inhibitory Activity Polypeptide 2	20	20	20	20	20	20	20	20
HG3513-HT3688, at	Wnt5b "Epithelial", Alt. Splice 8	20	20	20	20	20	20	20	20
HG3514-HT3688, at	Myosin "I", "Epithelial", Alt. Splice 8	70	390	390	390	390	390	390	390
HG3515-HT3688, at	Insulin-Like Growth Factor Receptor	20	20	20	20	20	20	20	20
HG3516-HT3688, at	Homeotic Protein Hox-6	20	20	20	20	20	20	20	20
HG3517-HT3688, at	Ycrone, Kcase Sx	32	32	32	32	32	32	32	32
HG3518-HT3688, at	Immunoglobulin Heavy Chain, VDJ Regions (Gp-L23566)	20	20	20	20	20	20	20	20
HG3519-HT3688, at	Immunoglobulin Heavy Chain, VDJ Regions (Gp-L23566)	20	20	20	20	20	20	20	20
HG3520-HT3688, at	Basic Transcription Factor 2, 34 Kda Subunit	20	20	20	20	20	20	20	20
HG3521-HT3688, at	Basic Transcription Factor 2, 44 Kda Subunit	20	20	20	20	20	20	20	20
HG3522-HT3688, at	Immunoglobulin Heavy Chain, Fc Fragment	20	20	20	20	20	20	20	20
HG3523-HT3688, at	Ribosomal Protein L26	1409	1634	1634	1634	1634	1634	1634	1634
HG3524-HT3688, at	Myo-4a Antigen	20	20	20	20	20	20	20	20
HG3525-HT3688, at	Immunoglobulin Gamma Heavy Chain, VDJ Regions (Gp-U13200)	20	20	20	20	20	20	20	20
HG3526-HT3688, at	Homeotic Protein Hox-42	20	20	20	20	20	20	20	20
HG3527-HT3688, at	Phosphoglucomutase 1, Alt. Splice	20	20	20	20	20	20	20	20
HG3528-HT3688, at	Botkin "Channel", Type "III", Alpha Subunit, Brain	20	20	20	20	20	20	20	20
HG3529-HT3688, at	Cell Division Cycle Protein 2-Related Protein Kinase (Pikase)	20	20	20	20	20	20	20	20
HG3530-HT3688, at	Homeotic Protein "A1", Class "I", Alt. Splice 1	20	20	20	20	20	20	20	20

Gene	Accession	Length	Score	Expect	Ident	Align	Gap	Start	End	Strand	Frame	Protein	Function	Ref
HG3921-IT4181_1	U01111	100	100	0.00	100	100	0	1	100	+	1	Homocysteine Protein "Cys" Class 1		1
HG3922-IT4182_1	U01112	100	100	0.00	100	100	0	1	100	+	1	Surfactant Protein Sp-A2 Delta		2
HG3923-IT4183_1	U01113	100	100	0.00	100	100	0	1	100	+	1	Surfactant Protein Sp-A1 Delta		3
HG3924-IT4184_1	U01114	100	100	0.00	100	100	0	1	100	+	1	Surfactant Protein Sp-A2 Delta		4
HG3925-IT4185_1	U01115	100	100	0.00	100	100	0	1	100	+	1	Surfactant Protein Sp-A1 Delta		5
HG3926-IT4186_1	U01116	100	100	0.00	100	100	0	1	100	+	1	Surfactant Protein Sp-A2 Delta		6
HG3927-IT4187_1	U01117	100	100	0.00	100	100	0	1	100	+	1	Surfactant Protein Sp-A1 Delta		7
HG3928-IT4188_1	U01118	100	100	0.00	100	100	0	1	100	+	1	Surfactant Protein Sp-A2 Delta		8
HG3929-IT4189_1	U01119	100	100	0.00	100	100	0	1	100	+	1	Surfactant Protein Sp-A1 Delta		9
HG3930-IT4190_1	U01120	100	100	0.00	100	100	0	1	100	+	1	Surfactant Protein Sp-A2 Delta		10
HG3931-IT4191_1	U01121	100	100	0.00	100	100	0	1	100	+	1	Surfactant Protein Sp-A1 Delta		11
HG3932-IT4192_1	U01122	100	100	0.00	100	100	0	1	100	+	1	Surfactant Protein Sp-A2 Delta		12
HG3933-IT4193_1	U01123	100	100	0.00	100	100	0	1	100	+	1	Surfactant Protein Sp-A1 Delta		13
HG3934-IT4194_1	U01124	100	100	0.00	100	100	0	1	100	+	1	Surfactant Protein Sp-A2 Delta		14
HG3935-IT4195_1	U01125	100	100	0.00	100	100	0	1	100	+	1	Surfactant Protein Sp-A1 Delta		15
HG3936-IT4196_1	U01126	100	100	0.00	100	100	0	1	100	+	1	Surfactant Protein Sp-A2 Delta		16
HG3937-IT4197_1	U01127	100	100	0.00	100	100	0	1	100	+	1	Surfactant Protein Sp-A1 Delta		17
HG3938-IT4198_1	U01128	100	100	0.00	100	100	0	1	100	+	1	Surfactant Protein Sp-A2 Delta		18
HG3939-IT4199_1	U01129	100	100	0.00	100	100	0	1	100	+	1	Surfactant Protein Sp-A1 Delta		19
HG3940-IT4200_1	U01130	100	100	0.00	100	100	0	1	100	+	1	Surfactant Protein Sp-A2 Delta		20
HG3941-IT4201_1	U01131	100	100	0.00	100	100	0	1	100	+	1	Surfactant Protein Sp-A1 Delta		21
HG3942-IT4202_1	U01132	100	100	0.00	100	100	0	1	100	+	1	Surfactant Protein Sp-A2 Delta		22
HG3943-IT4203_1	U01133	100	100	0.00	100	100	0	1	100	+	1	Surfactant Protein Sp-A1 Delta		23
HG3944-IT4204_1	U01134	100	100	0.00	100	100	0	1	100	+	1	Surfactant Protein Sp-A2 Delta		24
HG3945-IT4205_1	U01135	100	100	0.00	100	100	0	1	100	+	1	Surfactant Protein Sp-A1 Delta		25
HG3946-IT4206_1	U01136	100	100	0.00	100	100	0	1	100	+	1	Surfactant Protein Sp-A2 Delta		26
HG3947-IT4207_1	U01137	100	100	0.00	100	100	0	1	100	+	1	Surfactant Protein Sp-A1 Delta		27

[illegible]

[illegible]

[illegible]

[illegible]

[illegible]

124

Accession	Gene	Protein	Function	Length (aa)	Weight (kDa)	PI	Ref
U01568	Human alpha ribosomal protein L18 (RPL18)	"mRNA", complete cds		11568	21.70	5.22	1172
U01573	Human auricular protein B "mRNA", complete cds	igb-4, 11673	Myo-p-RNA	11573	20	20	20
U01574	Human deacylase transposase-like protein "mRNA", complete cds			11574	212	212	212
U01575	Human Kruppel related zinc finger protein (KRF10) "mRNA", complete cds			11575	1513	1513	1513
U01576	Human Kruppel related zinc finger protein (KRF10) "mRNA", complete cds			11576	1144	1144	1144
U01577	Human activin receptor-like kinase (ALK5) "mRNA", complete cds			11577	202	202	202
U01578	Human phospholipase D "mRNA", complete cds			11578	34	34	34
U01579	Human phospholipase D "mRNA", complete cds			11579	20	20	20
U01580	Human phospholipase D "mRNA", complete cds			11580	53	53	53
U01581	Human phospholipase D "mRNA", complete cds			11581	187	187	187
U01582	Human 17 beta hydroxysteroid dehydrogenase type 2 "mRNA", complete cds			11582	661	661	661
U01583	Human cytosolic serine hydroxymethyltransferase (SHMT) "mRNA", complete cds			11583	143	143	143
U01584	Human cAMP phosphodiesterase "mRNA", 3 and 7			11584	20	20	20
U01585	Human cAMP phosphodiesterase "mRNA", 3 and 7			11585	20	20	20
U01586	Human cAMP phosphodiesterase "mRNA", 3 and 7			11586	20	20	20
U01587	Human cAMP phosphodiesterase "mRNA", 3 and 7			11587	20	20	20
U01588	Human cAMP phosphodiesterase "mRNA", 3 and 7			11588	20	20	20
U01589	Human cAMP phosphodiesterase "mRNA", 3 and 7			11589	20	20	20
U01590	Human cAMP phosphodiesterase "mRNA", 3 and 7			11590	20	20	20
U01591	Human cAMP phosphodiesterase "mRNA", 3 and 7			11591	20	20	20
U01592	Human cAMP phosphodiesterase "mRNA", 3 and 7			11592	20	20	20
U01593	Human cAMP phosphodiesterase "mRNA", 3 and 7			11593	20	20	20
U01594	Human cAMP phosphodiesterase "mRNA", 3 and 7			11594	20	20	20
U01595	Human cAMP phosphodiesterase "mRNA", 3 and 7			11595	20	20	20
U01596	Human cAMP phosphodiesterase "mRNA", 3 and 7			11596	20	20	20
U01597	Human cAMP phosphodiesterase "mRNA", 3 and 7			11597	20	20	20
U01598	Human cAMP phosphodiesterase "mRNA", 3 and 7			11598	20	20	20
U01599	Human cAMP phosphodiesterase "mRNA", 3 and 7			11599	20	20	20
U01600	Human cAMP phosphodiesterase "mRNA", 3 and 7			11600	20	20	20
U01601	Human cAMP phosphodiesterase "mRNA", 3 and 7			11601	20	20	20
U01602	Human cAMP phosphodiesterase "mRNA", 3 and 7			11602	20	20	20
U01603	Human cAMP phosphodiesterase "mRNA", 3 and 7			11603	20	20	20
U01604	Human cAMP phosphodiesterase "mRNA", 3 and 7			11604	20	20	20
U01605	Human cAMP phosphodiesterase "mRNA", 3 and 7			11605	20	20	20
U01606	Human cAMP phosphodiesterase "mRNA", 3 and 7			11606	20	20	20
U01607	Human cAMP phosphodiesterase "mRNA", 3 and 7			11607	20	20	20
U01608	Human cAMP phosphodiesterase "mRNA", 3 and 7			11608	20	20	20
U01609	Human cAMP phosphodiesterase "mRNA", 3 and 7			11609	20	20	20
U01610	Human cAMP phosphodiesterase "mRNA", 3 and 7			11610	20	20	20
U01611	Human cAMP phosphodiesterase "mRNA", 3 and 7			11611	20	20	20
U01612	Human cAMP phosphodiesterase "mRNA", 3 and 7			11612	20	20	20
U01613	Human cAMP phosphodiesterase "mRNA", 3 and 7			11613	20	20	20
U01614	Human cAMP phosphodiesterase "mRNA", 3 and 7			11614	20	20	20
U01615	Human cAMP phosphodiesterase "mRNA", 3 and 7			11615	20	20	20
U01616	Human cAMP phosphodiesterase "mRNA", 3 and 7			11616	20	20	20
U01617	Human cAMP phosphodiesterase "mRNA", 3 and 7			11617	20	20	20

[illegible]

[illegible]

Accession	Gene	Chromosome	Start	End	Strand	Size	GC	GC3	GC4	GC5	GC6	GC7	GC8	GC9	GC10	GC11	GC12	GC13	GC14	GC15	GC16	GC17	GC18	GC19	GC20	GC21	GC22	GC23	GC24	GC25	GC26	GC27	GC28	GC29	GC30	GC31	GC32	GC33	GC34	GC35	GC36	GC37	GC38	GC39	GC40	GC41	GC42	GC43	GC44	GC45	GC46	GC47	GC48	GC49	GC50	GC51	GC52	GC53	GC54	GC55	GC56	GC57	GC58	GC59	GC60	GC61	GC62	GC63	GC64	GC65	GC66	GC67	GC68	GC69	GC70	GC71	GC72	GC73	GC74	GC75	GC76	GC77	GC78	GC79	GC80	GC81	GC82	GC83	GC84	GC85	GC86	GC87	GC88	GC89	GC90	GC91	GC92	GC93	GC94	GC95	GC96	GC97	GC98	GC99	GC100	GC101	GC102	GC103	GC104	GC105	GC106	GC107	GC108	GC109	GC110	GC111	GC112	GC113	GC114	GC115	GC116	GC117	GC118	GC119	GC120	GC121	GC122	GC123	GC124	GC125	GC126	GC127	GC128	GC129	GC130	GC131	GC132	GC133	GC134	GC135	GC136	GC137	GC138	GC139	GC140	GC141	GC142	GC143	GC144	GC145	GC146	GC147	GC148	GC149	GC150	GC151	GC152	GC153	GC154	GC155	GC156	GC157	GC158	GC159	GC160	GC161	GC162	GC163	GC164	GC165	GC166	GC167	GC168	GC169	GC170	GC171	GC172	GC173	GC174	GC175	GC176	GC177	GC178	GC179	GC180	GC181	GC182	GC183	GC184	GC185	GC186	GC187	GC188	GC189	GC190	GC191	GC192	GC193	GC194	GC195	GC196	GC197	GC198	GC199	GC200	GC201	GC202	GC203	GC204	GC205	GC206	GC207	GC208	GC209	GC210	GC211	GC212	GC213	GC214	GC215	GC216	GC217	GC218	GC219	GC220	GC221	GC222	GC223	GC224	GC225	GC226	GC227	GC228	GC229	GC230	GC231	GC232	GC233	GC234	GC235	GC236	GC237	GC238	GC239	GC240	GC241	GC242	GC243	GC244	GC245	GC246	GC247	GC248	GC249	GC250	GC251	GC252	GC253	GC254	GC255	GC256	GC257	GC258	GC259	GC260	GC261	GC262	GC263	GC264	GC265	GC266	GC267	GC268	GC269	GC270	GC271	GC272	GC273	GC274	GC275	GC276	GC277	GC278	GC279	GC280	GC281	GC282	GC283	GC284	GC285	GC286	GC287	GC288	GC289	GC290	GC291	GC292	GC293	GC294	GC295	GC296	GC297	GC298	GC299	GC300	GC301	GC302	GC303	GC304	GC305	GC306	GC307	GC308	GC309	GC310	GC311	GC312	GC313	GC314	GC315	GC316	GC317	GC318	GC319	GC320	GC321	GC322	GC323	GC324	GC325	GC326	GC327	GC328	GC329	GC330	GC331	GC332	GC333	GC334	GC335	GC336	GC337	GC338	GC339	GC340	GC341	GC342	GC343	GC344	GC345	GC346	GC347	GC348	GC349	GC350	GC351	GC352	GC353	GC354	GC355	GC356	GC357	GC358	GC359	GC360	GC361	GC362	GC363	GC364	GC365	GC366	GC367	GC368	GC369	GC370	GC371	GC372	GC373	GC374	GC375	GC376	GC377	GC378	GC379	GC380	GC381	GC382	GC383	GC384	GC385	GC386	GC387	GC388	GC389	GC390	GC391	GC392	GC393	GC394	GC395	GC396	GC397	GC398	GC399	GC400	GC401	GC402	GC403	GC404	GC405	GC406	GC407	GC408	GC409	GC410	GC411	GC412	GC413	GC414	GC415
-----------	------	------------	-------	-----	--------	------	----	-----	-----	-----	-----	-----	-----	-----	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------

[illegible]

[illegible]

[illegible]

[illegible]

Expressed RNA in Subcutaneous connective tissue, Normal urothelium and Transitional cell carcinoma										
Human placental protein (PPI) "mRNA", complete cds	67	20481	20	4900	20	3468	20	1906	20	1616
Human homologue of rat insulinoma gene ("ig") - exon 4-lan	32	111	20	20	20	105	20	77	20	66
Human MHC class II HLA-DR beta-1 mRNA (YDR2.3) - Sterd	20	20	20	20	20	20	20	66	20	20
Human muscle glycogen phosphorylase (PYGM) gene	20	20	20	20	20	20	20	20	20	20
Human salivary nucleolin "gene", 5' flank	20	20	20	20	20	20	20	20	20	20
Human steroid 11-beta-hydroxylase (CYP11B1) gene	66	46	20	353	219	219	20	44	20	44
Human insulin CP-Z2 "mRNA", complete cds	133	20	20	224	140	21	119	154	20	154
Human F-epsilon1 receptor gamma-chain "mRNA", complete cds	231	120	20	20	20	20	20	148	20	148
Human vesicular "mRNA", complete cds	20	60	20	20	20	20	20	39	20	184
Human cytochrome P450A4 (CYP2A4) "mRNA", complete cds	20	20	20	20	20	20	20	517	48	20
Human cytochrome P450A3 (CYP2A3) "mRNA", complete cds	217	136	365	232	117	20	20	20	20	20
Human CAMP-dependent protein kinase alpha subunit (PRKARIA) "mRNA", complete cds	40	24	20	20	20	20	20	20	20	20
Human cell adhesion protein (BQMI) "mRNA", complete cds	77	24	20	20	20	20	20	20	20	20
Human 2S-RNA phosphoprotein (BQMI) "mRNA", complete cds	313	40	20	20	20	20	20	20	20	20
Human tyrosine-kinase "cDNA", 5' end	142	109	20	20	20	20	20	20	20	20
Human HLA-B-associated transcript 2 (BAT2) "gene", 5' flank	20	20	20	20	20	20	20	20	20	20
Human HLA-B-associated transcript 3 (BAT3) "gene", 5' end	20	20	20	20	20	20	20	20	20	20
Human lymphocyte-specific protein 1 (LSP1) "mRNA", complete cds	818	395	20	20	20	20	20	20	20	20
Human MHC class II HLA-DQ beta-1 (DQB1) "mRNA", complete cds	20	20	20	20	20	20	20	20	20	20
Human (Gene 7) (H2-133) alpha-2 type IV collagen (COL4A2) "mRNA", complete cds	1423	267	20	20	20	20	20	20	20	20
Human 26-kDa cell surface protein TAPA-1 "mRNA", complete cds	66	61	146	254	1905	631	20	110	20	110
Human (Gene lambda-10-2) non-receptor tyrosine phosphatase 1 (PTEN1) gene	369	308	568	313	243	271	20	271	20	271
Human ornithine decarboxylase "gene", complete cds	66	33	20	20	20	20	20	20	20	20
Human fast skeletal muscle troponin C gene	31	34	35	20	20	20	20	20	20	20
Human p78 protein "mRNA", complete cds	517	287	300	619	1390	1256	20	131	20	131
Human carbonic anhydrase I (CAI) "mRNA", complete cds	145	123	194	141	84	52	20	20	20	20
Human alpha-2-macroglobulin receptor (alpha-2 m) "mRNA", complete cds	47	20	20	20	20	20	20	20	20	20
Human transforming growth factor-beta-1 binding protein "mRNA", complete cds	20	20	20	20	20	20	20	20	20	20
Human coe2545 "mRNA", complete cds	20	20	20	20	20	20	20	20	20	20
Human immunoglobulin heavy chain constant region (IgG1) "mRNA", complete cds	144	110	253	43	22	145	20	354	20	354
Human beta-tubulin "mRNA", complete cds	277	20	20	20	20	20	20	20	20	20
Human testis-specific cAMP-dependent protein kinase catalytic subunit (C-beta isoform) "mRNA", complete cds	924	772	1027	722	1221	1193	20	164	20	164
Human testis-specific protein kinase gamma subunit "mRNA", complete cds	30	158	104	98	903	275	20	20	20	20
Human laboratory-coat dehydrogenase (LD) "mRNA", complete cds	37	64	100	110	177	164	20	20	20	20
Human plasminogen gene	82	20	243	179	51	51	20	20	20	20
Human epidermal growth factor receptor (HER3) "mRNA", complete cds	42	33	93	78	20	20	20	20	20	20
Human spermidine synthase "mRNA", complete cds	81	128	20	58	107	94	20	20	20	20
Human placental protein 9 (PLP9) gene	67	85	107	56	283	20	20	20	20	20
Human transmembrane tyrosine-specific protein kinase (ROS1) "mRNA", complete cds	20	20	20	20	20	20	20	20	20	20
Human GAP-43 (GAP-43) beta-2-glycoprotein (GAP-43) gene	20	20	20	20	20	20	20	20	20	20
Human GAP-43 (GAP-43) beta-2-glycoprotein (GAP-43) gene	20	20	20	20	20	20	20	20	20	20
Human GAP-43 (GAP-43) beta-2-glycoprotein (GAP-43) gene	20	20	20	20	20	20	20	20	20	20
Human GAP-43 (GAP-43) beta-2-glycoprotein (GAP-43) gene	20	20	20	20	20	20	20	20	20	20
Human GAP-43 (GAP-43) beta-2-glycoprotein (GAP-43) gene	20	20	20	20	20	20	20	20	20	20
Human GAP-43 (GAP-43) beta-2-glycoprotein (GAP-43) gene	20	20	20	20	20	20	20	20	20	20
Human GAP-43 (GAP-43) beta-2-glycoprotein (GAP-43) gene	20	20	20	20	20	20	20	20	20	20
Human GAP-43 (GAP-43) beta-2-glycoprotein (GAP-43) gene	20	20	20	20	20	20	20	20	20	20
Human GAP-43 (GAP-43) beta-2-glycoprotein (GAP-43) gene	20	20	20	20	20	20	20	20	20	20
Human GAP-43 (GAP-43) beta-2-glycoprotein (GAP-43) gene	20	20	20	20	20	20	20	20	20	20
Human GAP-43 (GAP-43) beta-2-glycoprotein (GAP-43) gene	20	20	20	20	20	20	20	20	20	20
Human GAP-43 (GAP-43) beta-2-glycoprotein (GAP-43) gene	20	20	20	20	20	20	20	20	20	20
Human GAP-43 (GAP-43) beta-2-glycoprotein (GAP-43) gene	20	20	20	20	20	20	20	20	20	20
Human GAP-43 (GAP-43) beta-2-glycoprotein (GAP-43) gene	20	20	20	20	20	20	20	20	20	20
Human GAP-43 (GAP-43) beta-2-glycoprotein (GAP-43) gene	20	20	20	20	20	20	20	20	20	20
Human GAP-43 (GAP-43) beta-2-glycoprotein (GAP-43) gene	20	20	20	20	20	20	20	20	20	20
Human GAP-43 (GAP-43) beta-2-glycoprotein (GAP-43) gene	20	20	20	20	20	20	20	20	20	20
Human GAP-43 (GAP-43) beta-2-glycoprotein (GAP-43) gene	20	20	20	20	20	20	20	20	20	20
Human GAP-43 (GAP-43) beta-2-glycoprotein (GAP-43) gene	20	20	20	20	20	20	20	20	20	20
Human GAP-43 (GAP-43) beta-2-glycoprotein (GAP-43) gene	20	20	20	20	20	20	20	20	20	20
Human GAP-43 (GAP-43) beta-2-glycoprotein (GAP-43) gene	20	20	20	20	20	20	20	20	20	20
Human GAP-43 (GAP-43) beta-2-glycoprotein (GAP-43) gene	20	20	20	20	20	20	20	20	20	20
Human GAP-43 (GAP-43) beta-2-glycoprotein (GAP-43) gene	20	20	20	20	20	20	20	20	20	20
Human GAP-43 (GAP-43) beta-2-glycoprotein (GAP-43) gene	20	20	20	20	20	20	20	20	20	20
Human GAP-43 (GAP-43) beta-2-glycoprotein (GAP-43) gene	20	20	20	20	20	20	20	20	20	20
Human GAP-43 (GAP-43) beta-2-glycoprotein (GAP-43) gene	20	20	20	20	20	20	20	20	20	20
Human GAP-43 (GAP-43) beta-2-glycoprotein (GAP-43) gene	20	20	20	20	20	20	20	20	20	20
Human GAP-43 (GAP-43) beta-2-glycoprotein (GAP-43) gene	20	20	20	20	20	20	20	20	20	20
Human GAP-43 (GAP-43) beta-2-glycoprotein (GAP-43) gene	20	20	20	20	20	20	20	20	20	20
Human GAP-43 (GAP-43) beta-2-glycoprotein (GAP-43) gene	20	20	20	20	20	20	20	20	20	20
Human GAP-43 (GAP-43) beta-2-glycoprotein (GAP-43) gene	20	20	20	20	20	20	20	20	20	20
Human GAP-43 (GAP-43) beta-2-glycoprotein (GAP-43) gene	20	20	20	20	20	20	20	20	20	20
Human GAP-43 (GAP-43) beta-2-glycoprotein (GAP-43) gene	20	20	20	20	20	20	20	20	20	20
Human GAP-43 (GAP-43) beta-2-glycoprotein (GAP-43) gene	20	20	20	20	20	20	20	20	20	20
Human GAP-43 (GAP-43) beta-2-glycoprotein (GAP-43) gene	20	20	20	20	20	20	20	20	20	20
Human GAP-43 (GAP-43) beta-2-glycoprotein (GAP-43) gene	20	20	20	20	20	20	20	20	20	20
Human GAP-43 (GAP-43) beta-2-glycoprotein (GAP-43) gene	20	20	20	20	20	20	20	20	20	20
Human GAP-43 (GAP-43) beta-2-glycoprotein (GAP-43) gene	20	20	20	20	20	20	20	20	20</	

[illegible]

Expressed RNA in Subepithelial connective tissue, Normal urothelium and Transitional cell carcinomas

[illegible]

[illegible]

Expressed RNA in Eubacterial connective tissues, Normal urothelium and Translational cell carcinoma		228	229	230	231	232	233	234	235	236	237	238	239	240	241	242	243	244	245	246	247	248	249	250	251	252	253	254	255	256	257	258	259	260	261	262	263	264	265	266	267	268	269	270	271	272	273	274	275	276	277	278	279	280	281	282	283	284	285	286	287	288	289	290	291	292	293	294	295	296	297	298	299	300	301	302	303	304	305	306	307	308	309	310	311	312	313	314	315	316	317	318	319	320	321	322	323	324	325	326	327	328	329	330	331	332	333	334	335	336	337	338	339	340	341	342	343	344	345	346	347	348	349	350	351	352	353	354	355	356	357	358	359	360	361	362	363	364	365	366	367	368	369	370	371	372	373	374	375	376	377	378	379	380	381	382	383	384	385	386	387	388	389	390	391	392	393	394	395	396	397	398	399	400	401	402	403	404	405	406	407	408	409	410	411	412	413	414	415	416	417	418	419	420	421	422	423	424	425	426	427	428	429	430	431	432	433	434	435	436	437	438	439	440	441	442	443	444	445	446	447	448	449	450	451	452	453	454	455	456	457	458	459	460	461	462	463	464	465	466	467	468	469	470	471	472	473	474	475	476	477	478	479	480	481	482	483	484	485	486	487	488	489	490	491	492	493	494	495	496	497	498	499	500	501	502	503	504	505	506	507	508	509	510	511	512	513	514	515	516	517	518	519	520	521	522	523	524	525	526	527	528	529	530	531	532	533	534	535	536	537	538	539	540	541	542	543	544	545	546	547	548	549	550	551	552	553	554	555	556	557	558	559	560	561	562	563	564	565	566	567	568	569	570	571	572	573	574	575	576	577	578	579	580	581	582	583	584	585	586	587	588	589	590	591	592	593	594	595	596	597	598	599	600	601	602	603	604	605	606	607	608	609	610	611	612	613	614	615	616	617	618	619	620	621	622	623	624	625	626	627	628	629	630	631	632	633	634	635	636	637	638	639	640	641	642	643	644	645	646	647	648	649	650	651	652	653	654	655	656	657	658	659	660	661	662	663	664	665	666	667	668	669	670	671	672	673	674	675	676	677	678	679	680	681	682	683	684	685	686	687	688	689	690	691	692	693	694	695	696	697	698	699	700	701	702	703	704	705	706	707	708	709	710	711	712	713	714	715	716	717	718	719	720	721	722	723	724	725	726	727	728	729	730	731	732	733	734	735	736	737	738	739	740	741	742	743	744	745	746	747	748	749	750	751	752	753	754	755	756	757	758	759	760	761	762	763	764	765	766	767	768	769	770	771	772	773	774	775	776	777	778	779	780	781	782	783	784	785	786	787	788	789	790	791	792	793	794	795	796	797	798	799	800	801	802	803	804	805	806	807	808	809	810	811	812	813	814	815	816	817	818	819	820	821	822	823	824	825	826	827	828	829	830	831	832	833	834	835	836	837	838	839	840	841	842	843	844	845	846	847	848	849	850	851	852	853	854	855	856	857	858	859	860	861	862	863	864	865	866	867	868	869	870	871	872	873	874	875	876	877	878	879	880	881	882	883	884	885	886	887	888	889	890	891	892	893	894	895	896	897	898	899	900	901	902	903	904	905	906	907	908	909	910	911	912	913	914	915	916	917	918	919	920	921	922	923	924	925	926	927	928	929	930	931	932	933	934	935	936	937	938	939	940	941	942	943	944	945	946	947	948	949	950	951	952	953	954	955	956	957	958	959	960	961	962	963	964	965	966	967	968	969	970	971	972	973	974	975	976	977	978	979	980	981	982	983	984	985	986	987	988	989	990	991	992	993	994	995	996	997	998	999	1000
AB3483.at	Human major nuclear matrix protein mRNA																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																													</																																																																																																																																																																																																																																								

[illegible]

Gida 47

[illegible]

[illegible]

[illegible]

Accession	Gene	Chromosome	Start	End	Strand	Size	GC	GC3	GC4	GC5	GC6	GC7	GC8	GC9	GC10	GC11	GC12	GC13	GC14	GC15	GC16	GC17	GC18	GC19	GC20	GC21	GC22	GC23	GC24	GC25	GC26	GC27	GC28	GC29	GC30	GC31	GC32	GC33	GC34	GC35	GC36	GC37	GC38	GC39	GC40	GC41	GC42	GC43	GC44	GC45	GC46	GC47	GC48	GC49	GC50	GC51	GC52	GC53	GC54	GC55	GC56	GC57	GC58	GC59	GC60	GC61	GC62	GC63	GC64	GC65	GC66	GC67	GC68	GC69	GC70	GC71	GC72	GC73	GC74	GC75	GC76	GC77	GC78	GC79	GC80	GC81	GC82	GC83	GC84	GC85	GC86	GC87	GC88	GC89	GC90	GC91	GC92	GC93	GC94	GC95	GC96	GC97	GC98	GC99	GC100	GC101	GC102	GC103	GC104	GC105	GC106	GC107	GC108	GC109	GC110	GC111	GC112	GC113	GC114	GC115	GC116	GC117	GC118	GC119	GC120	GC121	GC122	GC123	GC124	GC125	GC126	GC127	GC128	GC129	GC130	GC131	GC132	GC133	GC134	GC135	GC136	GC137	GC138	GC139	GC140	GC141	GC142	GC143	GC144	GC145	GC146	GC147	GC148	GC149	GC150	GC151	GC152	GC153	GC154	GC155	GC156	GC157	GC158	GC159	GC160	GC161	GC162	GC163	GC164	GC165	GC166	GC167	GC168	GC169	GC170	GC171	GC172	GC173	GC174	GC175	GC176	GC177	GC178	GC179	GC180	GC181	GC182	GC183	GC184	GC185	GC186	GC187	GC188	GC189	GC190	GC191	GC192	GC193	GC194	GC195	GC196	GC197	GC198	GC199	GC200	GC201	GC202	GC203	GC204	GC205	GC206	GC207	GC208	GC209	GC210	GC211	GC212	GC213	GC214	GC215	GC216	GC217	GC218	GC219	GC220	GC221	GC222	GC223	GC224	GC225	GC226	GC227	GC228	GC229	GC230	GC231	GC232	GC233	GC234	GC235	GC236	GC237	GC238	GC239	GC240	GC241	GC242	GC243	GC244	GC245	GC246	GC247	GC248	GC249	GC250	GC251	GC252	GC253	GC254	GC255	GC256	GC257	GC258	GC259	GC260	GC261	GC262	GC263	GC264	GC265	GC266	GC267	GC268	GC269	GC270	GC271	GC272	GC273	GC274	GC275	GC276	GC277	GC278	GC279	GC280	GC281	GC282	GC283	GC284	GC285	GC286	GC287	GC288	GC289	GC290	GC291	GC292	GC293	GC294	GC295	GC296	GC297	GC298	GC299	GC300	GC301	GC302	GC303	GC304	GC305	GC306	GC307	GC308	GC309	GC310	GC311	GC312	GC313	GC314	GC315	GC316	GC317	GC318	GC319	GC320	GC321	GC322	GC323	GC324	GC325	GC326	GC327	GC328	GC329	GC330	GC331	GC332	GC333	GC334	GC335	GC336	GC337	GC338	GC339	GC340	GC341	GC342	GC343	GC344	GC345	GC346	GC347	GC348	GC349	GC350	GC351	GC352	GC353	GC354	GC355	GC356	GC357	GC358	GC359	GC360	GC361	GC362	GC363	GC364	GC365	GC366	GC367	GC368	GC369	GC370	GC371	GC372	GC373	GC374	GC375	GC376	GC377	GC378	GC379	GC380	GC381	GC382	GC383	GC384	GC385	GC386	GC387	GC388	GC389	GC390	GC391	GC392	GC393	GC394	GC395	GC396	GC397	GC398	GC399	GC400	GC401	GC402	GC403	GC404	GC405	GC406	GC407	GC408	GC409	GC410	GC411	GC412	GC413	GC414	GC415
-----------	------	------------	-------	-----	--------	------	----	-----	-----	-----	-----	-----	-----	-----	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------

[illegible]

[illegible]

[illegible]

[illegible]

[illegible]

[illegible]

Page 85

Slide 67

167

[illegible]

Slide 70

[illegible]

171

[illegible]

[illegible]

Accession	Gene	Chromosome	Start	End	Strand	Size	GC	GC3	GC4	GC5	GC6	GC7	GC8	GC9	GC10	GC11	GC12	GC13	GC14	GC15	GC16	GC17	GC18	GC19	GC20	GC21	GC22	GC23	GC24	GC25	GC26	GC27	GC28	GC29	GC30	GC31	GC32	GC33	GC34	GC35	GC36	GC37	GC38	GC39	GC40	GC41	GC42	GC43	GC44	GC45	GC46	GC47	GC48	GC49	GC50	GC51	GC52	GC53	GC54	GC55	GC56	GC57	GC58	GC59	GC60	GC61	GC62	GC63	GC64	GC65	GC66	GC67	GC68	GC69	GC70	GC71	GC72	GC73	GC74	GC75	GC76	GC77	GC78	GC79	GC80	GC81	GC82	GC83	GC84	GC85	GC86	GC87	GC88	GC89	GC90	GC91	GC92	GC93	GC94	GC95	GC96	GC97	GC98	GC99	GC100	GC101	GC102	GC103	GC104	GC105	GC106	GC107	GC108	GC109	GC110	GC111	GC112	GC113	GC114	GC115	GC116	GC117	GC118	GC119	GC120	GC121	GC122	GC123	GC124	GC125	GC126	GC127	GC128	GC129	GC130	GC131	GC132	GC133	GC134	GC135	GC136	GC137	GC138	GC139	GC140	GC141	GC142	GC143	GC144	GC145	GC146	GC147	GC148	GC149	GC150	GC151	GC152	GC153	GC154	GC155	GC156	GC157	GC158	GC159	GC160	GC161	GC162	GC163	GC164	GC165	GC166	GC167	GC168	GC169	GC170	GC171	GC172	GC173	GC174	GC175	GC176	GC177	GC178	GC179	GC180	GC181	GC182	GC183	GC184	GC185	GC186	GC187	GC188	GC189	GC190	GC191	GC192	GC193	GC194	GC195	GC196	GC197	GC198	GC199	GC200	GC201	GC202	GC203	GC204	GC205	GC206	GC207	GC208	GC209	GC210	GC211	GC212	GC213	GC214	GC215	GC216	GC217	GC218	GC219	GC220	GC221	GC222	GC223	GC224	GC225	GC226	GC227	GC228	GC229	GC230	GC231	GC232	GC233	GC234	GC235	GC236	GC237	GC238	GC239	GC240	GC241	GC242	GC243	GC244	GC245	GC246	GC247	GC248	GC249	GC250	GC251	GC252	GC253	GC254	GC255	GC256	GC257	GC258	GC259	GC260	GC261	GC262	GC263	GC264	GC265	GC266	GC267	GC268	GC269	GC270	GC271	GC272	GC273	GC274	GC275	GC276	GC277	GC278	GC279	GC280	GC281	GC282	GC283	GC284	GC285	GC286	GC287	GC288	GC289	GC290	GC291	GC292	GC293	GC294	GC295	GC296	GC297	GC298	GC299	GC300	GC301	GC302	GC303	GC304	GC305	GC306	GC307	GC308	GC309	GC310	GC311	GC312	GC313	GC314	GC315	GC316	GC317	GC318	GC319	GC320	GC321	GC322	GC323	GC324	GC325	GC326	GC327	GC328	GC329	GC330	GC331	GC332	GC333	GC334	GC335	GC336	GC337	GC338	GC339	GC340	GC341	GC342	GC343	GC344	GC345	GC346	GC347	GC348	GC349	GC350	GC351	GC352	GC353	GC354	GC355	GC356	GC357	GC358	GC359	GC360	GC361	GC362	GC363	GC364	GC365	GC366	GC367	GC368	GC369	GC370	GC371	GC372	GC373	GC374	GC375	GC376	GC377	GC378	GC379	GC380	GC381	GC382	GC383	GC384	GC385	GC386	GC387	GC388	GC389	GC390	GC391	GC392	GC393	GC394	GC395	GC396	GC397	GC398	GC399	GC400	GC401	GC402	GC403	GC404	GC405	GC406	GC407	GC408	GC409	GC410	GC411	GC412	GC413	GC414	GC415
-----------	------	------------	-------	-----	--------	------	----	-----	-----	-----	-----	-----	-----	-----	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------

175

[illegible]

[illegible]

[illegible]

[illegible]

[illegible]

[illegible]

Accession	Gene	Size (bp)	GC (%)	GC3 (%)	GC4 (%)	GC5 (%)	GC6 (%)	GC7 (%)	GC8 (%)	GC9 (%)	GC10 (%)	GC11 (%)	GC12 (%)	GC13 (%)	GC14 (%)	GC15 (%)	GC16 (%)	GC17 (%)	GC18 (%)	GC19 (%)	GC20 (%)	GC21 (%)	GC22 (%)	GC23 (%)	GC24 (%)	GC25 (%)	GC26 (%)	GC27 (%)	GC28 (%)	GC29 (%)	GC30 (%)	GC31 (%)	GC32 (%)	GC33 (%)	GC34 (%)	GC35 (%)	GC36 (%)	GC37 (%)	GC38 (%)	GC39 (%)	GC40 (%)	GC41 (%)	GC42 (%)	GC43 (%)	GC44 (%)	GC45 (%)	GC46 (%)	GC47 (%)	GC48 (%)	GC49 (%)	GC50 (%)	GC51 (%)	GC52 (%)	GC53 (%)	GC54 (%)	GC55 (%)	GC56 (%)	GC57 (%)	GC58 (%)	GC59 (%)	GC60 (%)	GC61 (%)	GC62 (%)	GC63 (%)	GC64 (%)	GC65 (%)	GC66 (%)	GC67 (%)	GC68 (%)	GC69 (%)	GC70 (%)	GC71 (%)	GC72 (%)	GC73 (%)	GC74 (%)	GC75 (%)	GC76 (%)	GC77 (%)	GC78 (%)	GC79 (%)	GC80 (%)	GC81 (%)	GC82 (%)	GC83 (%)	GC84 (%)	GC85 (%)	GC86 (%)	GC87 (%)	GC88 (%)	GC89 (%)	GC90 (%)	GC91 (%)	GC92 (%)	GC93 (%)	GC94 (%)	GC95 (%)	GC96 (%)	GC97 (%)	GC98 (%)	GC99 (%)	GC100 (%)	GC101 (%)	GC102 (%)	GC103 (%)	GC104 (%)	GC105 (%)	GC106 (%)	GC107 (%)	GC108 (%)	GC109 (%)	GC110 (%)	GC111 (%)	GC112 (%)	GC113 (%)	GC114 (%)	GC115 (%)	GC116 (%)	GC117 (%)	GC118 (%)	GC119 (%)	GC120 (%)	GC121 (%)	GC122 (%)	GC123 (%)	GC124 (%)	GC125 (%)	GC126 (%)	GC127 (%)	GC128 (%)	GC129 (%)	GC130 (%)	GC131 (%)	GC132 (%)	GC133 (%)	GC134 (%)	GC135 (%)	GC136 (%)	GC137 (%)	GC138 (%)	GC139 (%)	GC140 (%)	GC141 (%)	GC142 (%)	GC143 (%)	GC144 (%)	GC145 (%)	GC146 (%)	GC147 (%)	GC148 (%)	GC149 (%)	GC150 (%)	GC151 (%)	GC152 (%)	GC153 (%)	GC154 (%)	GC155 (%)	GC156 (%)	GC157 (%)	GC158 (%)	GC159 (%)	GC160 (%)	GC161 (%)	GC162 (%)	GC163 (%)	GC164 (%)	GC165 (%)	GC166 (%)	GC167 (%)	GC168 (%)	GC169 (%)	GC170 (%)	GC171 (%)	GC172 (%)	GC173 (%)	GC174 (%)	GC175 (%)	GC176 (%)	GC177 (%)	GC178 (%)	GC179 (%)	GC180 (%)	GC181 (%)	GC182 (%)	GC183 (%)	GC184 (%)	GC185 (%)	GC186 (%)	GC187 (%)	GC188 (%)	GC189 (%)	GC190 (%)	GC191 (%)	GC192 (%)	GC193 (%)	GC194 (%)	GC195 (%)	GC196 (%)	GC197 (%)	GC198 (%)	GC199 (%)	GC200 (%)	GC201 (%)	GC202 (%)	GC203 (%)	GC204 (%)	GC205 (%)	GC206 (%)	GC207 (%)	GC208 (%)	GC209 (%)	GC210 (%)	GC211 (%)	GC212 (%)	GC213 (%)	GC214 (%)	GC215 (%)	GC216 (%)	GC217 (%)	GC218 (%)	GC219 (%)	GC220 (%)	GC221 (%)	GC222 (%)	GC223 (%)	GC224 (%)	GC225 (%)	GC226 (%)	GC227 (%)	GC228 (%)	GC229 (%)	GC230 (%)	GC231 (%)	GC232 (%)	GC233 (%)	GC234 (%)	GC235 (%)	GC236 (%)	GC237 (%)	GC238 (%)	GC239 (%)	GC240 (%)	GC241 (%)	GC242 (%)	GC243 (%)	GC244 (%)	GC245 (%)	GC246 (%)	GC247 (%)	GC248 (%)	GC249 (%)	GC250 (%)	GC251 (%)	GC252 (%)	GC253 (%)	GC254 (%)	GC255 (%)	GC256 (%)	GC257 (%)	GC258 (%)	GC259 (%)	GC260 (%)	GC261 (%)	GC262 (%)	GC263 (%)	GC264 (%)	GC265 (%)	GC266 (%)	GC267 (%)	GC268 (%)	GC269 (%)	GC270 (%)	GC271 (%)	GC272 (%)	GC273 (%)	GC274 (%)	GC275 (%)	GC276 (%)	GC277 (%)	GC278 (%)	GC279 (%)	GC280 (%)	GC281 (%)	GC282 (%)	GC283 (%)	GC284 (%)	GC285 (%)	GC286 (%)	GC287 (%)	GC288 (%)	GC289 (%)	GC290 (%)	GC291 (%)	GC292 (%)	GC293 (%)	GC294 (%)	GC295 (%)	GC296 (%)	GC297 (%)	GC298 (%)	GC299 (%)	GC300 (%)	GC301 (%)	GC302 (%)	GC303 (%)	GC304 (%)	GC305 (%)	GC306 (%)	GC307 (%)	GC308 (%)	GC309 (%)	GC310 (%)	GC311 (%)	GC312 (%)	GC313 (%)	GC314 (%)	GC315 (%)	GC316 (%)	GC317 (%)	GC318 (%)	GC319 (%)	GC320 (%)	GC321 (%)	GC322 (%)	GC323 (%)	GC324 (%)	GC325 (%)	GC326 (%)	GC327 (%)	GC328 (%)	GC329 (%)	GC330 (%)	GC331 (%)	GC332 (%)	GC333 (%)	GC334 (%)	GC335 (%)	GC336 (%)	GC337 (%)	GC338 (%)	GC339 (%)	GC340 (%)	GC341 (%)	GC342 (%)	GC343 (%)	GC344 (%)	GC345 (%)	GC346 (%)	GC347 (%)	GC348 (%)	GC349 (%)	GC350 (%)	GC351 (%)	GC352 (%)	GC353 (%)	GC354 (%)	GC355 (%)	GC356 (%)	GC357 (%)	GC358 (%)	GC359 (%)	GC360 (%)	GC361 (%)	GC362 (%)	GC363 (%)	GC364 (%)	GC365 (%)	GC366 (%)	GC367 (%)	GC368 (%)	GC369 (%)	GC370 (%)	GC371 (%)	GC372 (%)	GC373 (%)	GC374 (%)	GC375 (%)	GC376 (%)	GC377 (%)	GC378 (%)	GC379 (%)	GC380 (%)
-----------	------	-----------	--------	---------	---------	---------	---------	---------	---------	---------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------

of streptococcal RNA in subcutaneous connective tissue, normal urothelium and transitional cell carcinoma

194

[illegible]

[illegible]

[illegible]

[illegible]

[illegible]

Genbank	Gene ID	Gene name	covariance
AB000584_at	AB000584	TGF-beta superfamily protein,	av dif neg
AB002533_at	KPNA4	Qip1, :karyopherin alpha 4	av dif neg
AB002559_at	AB002559	hunc18b2,	av dif neg
AB003102_at	AB003102	26S proteasome subunit p44.5,	av dif neg
AB006782_at	AB006782	galectin-9 isoform,	av dif neg
AC002045_xpt2_s_at	AC002045	Chromosome 16 BAC clone CIT987	av dif neg
AC002073_cds1_at	AC002073	PAC clone DJ515N1 from 22q11.2	av dif neg
AC002115_cds1_at	AC002115	DNA from overlapping chromosom	av dif neg
AC002115_cds4_at	AC002115	DNA from overlapping chromosom	av dif neg
AD000082_cds1_at	CH19HHR23	DNA from chromosome 19p13.2 co	av dif neg
AF000562_at	AF000562	uroplakin II mRNA,	av dif neg
AF001359_f_at	AF001359	DNA mismatch repair protein \	av dif neg
AF009368_at	AF009368	Luman mRNA, :Luman "mRNA," /	av dif neg
AF015913_at	SKB1	SKB1Hs mRNA, :skb1 \S. pombe	av dif neg
D00017_at	HUMLIC	lipocortin II, :annexin II	av dif neg
D00408_s_at	HUMXYPFLA	fetal liver cytochrome P-450	av dif neg
D00596_at	HUMTS1	gene for thymidylate synthase,	av dif neg
D00654_at	HUMACTSG7	gene for enteric smooth muscle	av dif neg
D10523_at	HUM2OGDH	2-oxoglutarate dehydrogenase,	av dif neg
D11086_at	HUMIL2RG	interleukin 2 receptor gamma	av dif neg
D11086_at	HUMIL2RG	interleukin 2 receptor gamma	av dif neg
D11094_at	HUMMSS1	MSS1, :proteasome \prosome,	av dif neg
D11327_s_at	HUMLCPTP	protein-tyrosine phosphatase,	av dif neg
D13118_at	HUMATPSCP1	P1 ATP synthase subunit c, :	av dif neg
D13413_ma1_s_at	HUMTA120	tumor-associated 120 kDa nucl	av dif neg
D13843_at	HUMRSC390	KIAA0018 gene, :KIAA0018 gen	av dif neg
D13705_s_at	HUMOMHY	fatty acids omega-hydroxylase	av dif neg
D13748_at	HUM4AI	eukaryotic initiation factor	av dif neg
D14043_at	HUMMGC24	MGC-24, : "MGC-24," complete	av dif neg
D14530_at	HUMRSPT	homolog of yeast ribosomal pro	av dif neg
D14710_at	HUMIPASAS2	ATP synthase alpha subunit,	av dif neg
D16294_at	HUMDSAEC	mitochondrial 3-oxoacyl-CoA t	av dif neg
D16562_at	HUMATPSGL	ATP synthase gamma-subunit \	av dif neg
D16581_at	HUM8ODGTP	8-oxo-dGTPase, : "8-oxo-dGTP	av dif neg
D17516_at	HUMPACAPR	PACAP receptor, :adenylate c	av dif neg
D17516_at	HUMPACAPR	PACAP receptor, :adenylate c	av dif neg
D17525_at	D17525	precursor of P100 serine prot	av dif neg
D21063_at	HUMORFAAA	KIAA0030 gene,	av dif neg
D21261_at	HUMORFFA	KIAA0120 gene, :transgelin 2	av dif neg
D23660_at	HUMRSP	ribosomal protein, : ribosom	av dif neg
D25218_at	HUMORFN	KIAA0112 gene,	av dif neg
D25218_at	HUMORFN	KIAA0112 gene,	av dif neg
D25248_at	HUMRES44	mRNA, clone:RES4-4.	av dif neg
D25248_at	HUMRES44	mRNA, clone:RES4-4.	av dif neg
D25278_at	HUMORFO	KIAA0036 gene, :KIAA0036 gen	av dif neg
D25303_at	HUMIAS	Integrin alpha subunit,	av dif neg
D26129_at	HUMRNASA	ribonuclease A \RNase A\),	av dif neg
D26528_at	HUMRNA	RNA helicase, :DEAD/H \Asp-	av dif neg
D26535_s_at	HUMDS	gene for dihydrolipoamide succ	av dif neg
D26599_at	HUMPSH2	proteasome subunit HsC7-1, :	av dif neg
D28383_at	HUMASB42	ATP synthase B chain, 5'UTR	av dif neg
D28589_at	HUMKG1E	mRNA \KIAA00167\), partial se	av dif neg
D28915_at	HUMHCAMAP8	gene for hepatitis C-associate	av dif neg
D29012_at	HUMPSY	proteasome subunit Y, : prot	av dif neg

D29841_at	HUMORFA02	KIAA0052 gene,	av dif neg
D29958_at	HUMORFA10	KIAA0116 gene,	av dif neg
D30855_at	HUMELF4AII	eukaryotic initiation factor	av dif neg
D31764_at	HUMORFKG1C	KIAA0084 gene, :KIAA0084 gen	av dif neg
D31764_at	HUMORFKG1C	KIAA0084 gene, :KIAA0084 gen	av dif neg
D31883_at	HUMORFKG1L	KIAA0059 gene, : KIAA0059 "g	av dif neg
D31884_at	HUMORFKG1M	KIAA0083 gene, :KIAA0083 gen	av dif neg
D31884_at	HUMORFKG1M	KIAA0083 gene, :KIAA0083 gen	av dif neg
D31891_at	HUMORFKG1T	KIAA0087 gene, :SET domain,	av dif neg
D32129_f_at	HUMHLAAD	HLA class-I \\\(HLA-A26\\) heavy	av dif neg
D38047_at	HUMPSP31	28S proteasome subunit p31,	av dif neg
D38555_at	HUMORF008	KIAA0079 gene, :Sec24p, S. C	av dif neg
D38583_at	HUMCOLO	calgizzarin, : "calgizzarin,	av dif neg
D42048_at	HUMKIAAJ	KIAA0083 gene, :DNA2 \\\(DNA r	av dif neg
D42048_at	HUMKIAAJ	KIAA0083 gene, :DNA2 \\\(DNA r	av dif neg
D42047_at	HUMKIAAK	KIAA0089 gene, : KIAA0089 "g	av dif neg
D43682_s_at	HUMVLCAD	very-long-chain acyl-CoA dehy	av dif neg
D45370_at	HUMUPST1	apM2 GS2374 \\\(unknown product	av dif neg
D49396_at	HUMAOP1	Apo1_\\(MER5\\(Aop1-Mouse\\)-lik	av dif neg
D49488_at	HUMHTTP	alpha-tocopherol transfer pro	av dif neg
D49728_at	HUMNAK1	NAK1 DNA binding protein,	av dif neg
D49824_s_at	HUMHLABAA	HLA-B null allele mRNA. :HLA-B	av dif neg
D50840_at	D50825S16	DNA for phosphodiesterase 3B,	av dif neg
D63478_at	KIAA0144	KIAA0144 gene, :KIAA0144 gen	av dif neg
D63479_s_at	D63479	KIAA0145 gene,	av dif neg
D63485_at	KIAA0151	KIAA0151 gene, :KIAA0151 gen	av dif neg
D63486_at	KIAA0152	KIAA0152 gene, :KIAA0152 gen	av dif neg
D63851_at	D63851	unc-18 homologue,	av dif neg
D78129_at	HUMHL1115B	squalene epoxidase,	av dif neg
D78275_at	PSMC6	proteasome subunit p42, :pro	av dif neg
D79205_at	D79205	ribosomal protein L39,	av dif neg
D79984_s_at	D79984	KIAA0162 gene,	av dif neg
D79984_s_at	D79984	KIAA0162 gene,	av dif neg
D80002_at	D80002	KIAA0180 gene,	av dif neg
D82345_at	D82345	NB thymosin beta,	av dif neg
D86425_at	D86425	osteonidogen,	av dif neg
D86974_at	D86974	KIAA0220 gene, : " KIAA0220 "	av dif neg
D86985_at	KIAA0232	KIAA0232 gene, :KIAA0232 gen	av dif neg
D87258_at	D87258	serin protease with IGF-blndi	av dif neg
D87735_at	RPL14	ribosomal protein L14, :ribo	av dif neg
D87953_at	D87953	RTP, : "RTP," complete cds	av dif neg
D89052_at	ATP6F	proton-ATPase-like protein,	av dif neg
HG1034-HT1034_f_at	<empty>	<empty>	av dif neg
HG1400-HT1400_s_at	<empty>	<empty>	av dif neg
HG1428-HT1428_s_at	HG1428-HT1428	: ""Globin, "" Beta"	av dif neg
HG1428-HT1428_s_at	HG1428-HT1428	: ""Globin, "" Beta"	av dif neg
HG1515-HT1515_f_at	HG1515-HT1515	:Transcription Factor Btf3b	av dif neg
HG1515-HT1515_f_at	HG1515-HT1515	:Transcription Factor Btf3b	av dif neg
HG1614-HT1614_at	HG1614-HT1614	:Protein Phosphatase "1," Alp	av dif neg
HG1614-HT1614_at	HG1614-HT1614	:Protein Phosphatase "1," Alp	av dif neg
HG1800-HT1823_at	<empty>	<empty>	av dif neg
HG1872-HT1907_at	<empty>	<empty>	av dif neg
HG1872-HT1907_at	<empty>	<empty>	av dif neg
HG1980-HT2023_at	<empty>	<empty>	av dif neg
HG2147-HT2217_r_at	<empty>	<empty>	av dif neg

HG2147-HT2217_r_at	<empty>	<empty>	av dif neg
HG2149-HT2219_at	<empty>	<empty>	av dif neg
HG2167-HT2237_at	<empty>	<empty>	av dif neg
HG2197-HT2267_s_at	HG2197-HT2267	:Collage, Type Vii,	av dif neg
HG2238-HT2321_s_at	HG2238-HT2321	:Nuclear Mitotic Apparatus P	av dif neg
HG2239-HT2324_r_at	<empty>	<empty>	av dif neg
HG2239-HT2324_r_at	<empty>	<empty>	av dif neg
HG2264-HT2360_at	<empty>	<empty>	av dif neg
HG2279-HT2375_at	HG2279-HT2375	:Triosephosphate Isomerase	av dif neg
HG2566-HT4867_at	HG2566-HT4867	:Microtubule-Associated Prote	av dif neg
HG2788-HT2896_at	HG2788-HT2896	:Calcyclin	av dif neg
HG2815-HT2931_at	<empty>	<empty>	av dif neg
HG2815-HT2931_s_at	<empty>	<empty>	av dif neg
HG2815-HT4023_s_at	<empty>	<empty>	av dif neg
HG2873-HT3017_at	<empty>	<empty>	av dif neg
HG2917-HT3061_f_at	HG2917-HT3061	:Major Histocompatibility "	av dif neg
HG2917-HT3061_f_at	HG2917-HT3061	:Major Histocompatibility "	av dif neg
HG2981-HT3127_s_at	<empty>	<empty>	av dif neg
HG2994-HT4850_s_at	<empty>	<empty>	av dif neg
HG3039-HT3200_at	<empty>	<empty>	av dif neg
HG3076-HT3238_s_at	HG3076-HT3238	:Heterogeneous Nuclear Ribon	av dif neg
HG3107-HT3283_s_at	<empty>	<empty>	av dif neg
HG3107-HT3283_s_at	<empty>	<empty>	av dif neg
HG311-HT311_at	<empty>	<empty>	av dif neg
HG3214-HT3391_at	<empty>	<empty>	av dif neg
HG3236-HT3413_f_at	<empty>	<empty>	av dif neg
HG3254-HT3431_at	<empty>	<empty>	av dif neg
HG3342-HT3519_s_at	HG3342-HT3519	:Id1	av dif neg
HG3384-HT3541_at	HG3384-HT3541	:Ribosomal Protein L37	av dif neg
HG33-HT33_at	HG33-HT33	<empty>	av dif neg
HG3484-HT3678_s_at	<empty>	<empty>	av dif neg
HG3514-HT3708_at	HG3514-HT3708	:Tropomyosin Tm30nm, Cytosk	av dif neg
HG3543-HT3739_at	HG3543-HT3739	:Insulin-Like Growth Factor 2	av dif neg
HG3543-HT3739_at	HG3543-HT3739	:Insulin-Like Growth Factor 2	av dif neg
HG3549-HT3751_at	HG3549-HT3751	:Wilms Tumor-Related Protein	av dif neg
HG3570-HT3773_at	HG3570-HT3773	:Protein Phosphatase Inhibito	av dif neg
HG3576-HT3779_f_at	<empty>	<empty>	av dif neg
HG3576-HT3779_f_at	<empty>	<empty>	av dif neg
HG3731-HT4001_at	<empty>	<empty>	av dif neg
HG384-HT384_at	HG384-HT384	:Ribosomal Protein L26	av dif neg
HG384-HT384_at	HG384-HT384	:Ribosomal Protein L26	av dif neg
HG3945-HT4215_at	<empty>	<empty>	av dif neg
HG3991-HT4261_r_at	<empty>	<empty>	av dif neg
HG4020-HT4290_s_at	HG4020-HT4290	:Transglutaminase	av dif neg
HG4258-HT4528_at	<empty>	<empty>	av dif neg
HG4319-HT4589_at	HG4319-HT4589	:Ribosomal Protein L5	av dif neg
HG4338-HT4806_at	<empty>	<empty>	av dif neg
HG4533-HT4938_at	<empty>	<empty>	av dif neg
HG4542-HT4947_at	HG4542-HT4947	:Ribosomal Protein L10	av dif neg
HG4557-HT4962_r_at	<empty>	<empty>	av dif neg
HG4668-HT5083_s_at	<empty>	<empty>	av dif neg
HG4668-HT5083_s_at	<empty>	<empty>	av dif neg
HG4749-HT5197_at	<empty>	<empty>	av dif neg
HG613-HT613_at	HG613-HT613	:Ribosomal Protein S12	av dif neg
HG613-HT613_at	HG613-HT613	:Ribosomal Protein S12	av dif neg

HG821-HT821_at	<empty>	<empty>	av dif neg
HG880-HT880_at	<empty>	<empty>	av dif neg
HG880-HT880_at	<empty>	<empty>	av dif neg
HG987-HT987_at	HG987-HT987	:Mac25 :Mac25	av dif neg
J00105_s_at	HSMGLO	messenger RNA fragment for the	av dif neg
J02811_at	HUMAPOD	apolipoprotein D mRNA, :apoli	av dif neg
J02811_at	HUMAPOD	apolipoprotein D mRNA, :apoli	av dif neg
J02683_s_at	HUMATPC	ADP/ATP carrier protein mRNA,	av dif neg
J02783_at	HUMTHBP	thyroid hormone binding protei	av dif neg
J02874_at	HUMALBP	adipocyte lipid-binding protei	av dif neg
J02874_at	HUMALBP	adipocyte lipid-binding protei	av dif neg
J02902_at	HUMP2A	protein phosphatase 2A regulat	av dif neg
J02908_at	HUMCYPIIF	cytochrome P450IIF1 protein \	av dif neg
J03077_s_at	HUMGLBA	co-beta glucosidase \proactiv	av dif neg
J03242_s_at	HUMGFIL2	insulin-like growth factor II m	av dif neg
J03242_s_at	HUMGFIL2	insulin-like growth factor II m	av dif neg
J03592_at	HUMTLCA	ADP/ATP translocase mRNA, 3' e	av dif neg
J03758_at	HUMGHVA	growth hormone-variant \GH1\)	av dif neg
J03801_f_at	HUMLSZ	lysozyme mRNA, complete cds wi	av dif neg
J03909_at	HUMIIP	gamma-interferon-inducible pro	av dif neg
J03909_at	HUMIIP	gamma-interferon-inducible pro	av dif neg
J03934_s_at	HUMNMOR	Human, NAD(P)H:menadione oxi	av dif neg
J04093_s_at	HUMUGT1FA	phenol UDP-glucuronosyltransfe	av dif neg
J04093_s_at	HUMUGT1FA	phenol UDP-glucuronosyltransfe	av dif neg
J04152_ma1_s_at	HUMGA733A	gastrointestinal tumor-associa	av dif neg
J04164_at	HUM927A	interferon-inducible protein 9	av dif neg
J04164_at	HUM927A	interferon-inducible protein 9	av dif neg
J04173_at	HUMPGAM	phosphoglycerate mutase \PGAM	av dif neg
J04611_at	HUMANP70	lupus p70 \Ku\ autoantigen p	av dif neg
J04615_at	HUMSNRAA	lupus autoantigen \small nucl	av dif neg
J04617_s_at	HUMEF1A	elongation factor EF-1-alpha g	av dif neg
J04873_at	HUMCOR2M	cytochrome bc-1 complex core p	av dif neg
J05036_s_at	HUMCTSE	cathepsin E mRNA, :cathepsin	av dif neg
J05036_s_at	HUMCTSE	cathepsin E mRNA, :cathepsin	av dif neg
J05272_at	HUMIMPH	IMP dehydrogenase type 1 mRNA	av dif neg
K02405_f_at	HUMMHDC3B	MHC class II HLA-DC-3-beta gen	av dif neg
K03189_f_at	HUMCGBEL03	chorionic gonadotropin beta su	av dif pos
K03430_at	HUMC1QB2	complement C1q B-chain gene, e	av dif pos
K03430_at	HUMC1QB2	complement C1q B-chain gene, e	av dif pos
L00634_s_at	HUMFPTA	farnesyl-protein transferase a	av dif pos
L02328_f_at	HUMPREBLYM	\clone Hu lambda-17\ lambda-	av dif pos
L04270_at	HUMTNFRRP	\clone CD18\ tumor necrosis	av dif pos
L04483_s_at	HUMRPS21X	ribosomal protein S21 \RPS21	av dif pos
L04490_at	HUMNADH	\clone CC6\ NADH-ubiquinone	av dif pos
L05072_s_at	HUMIFNRF1A	interferon regulatory factor 1	av dif pos
L05188_f_at	HUMSPRR2B	small proline-rich protein 2	av dif pos
L06499_at	HUMRPL37A	ribosomal protein L37a \RPL37	av dif pos
L06505_at	HUML12A	ribosomal protein L12 mRNA, :	av dif pos
L06797_s_at	HUMGPCR	\clone L5\ orphan G protein-	av dif pos
L06797_s_at	HUMGPCR	\clone L5\ orphan G protein-	av dif pos
L07044_at	HUMCCDPKB	calcium/calmodulin-dependent p	av dif pos
L08666_at	HUMPORIN	porin \por\ mRNA, complete c	av dif pos
L09209_s_at	HUMAMYLOID	amyloid protein homologue mRNA	av dif pos
L10413_at	HUMFTA	farnesyltransferase alpha-subu	av dif pos
L11566_at	HUMRPL18A	ribosomal protein L18 \RPL18	av dif pos

L11672_at	HUMKRUPZN	Kruppel related zinc finger pr	av dif pos
L11708_at	HUMB17HSD	17 beta hydroxysteroid dehydro	av dif pos
L11708_at	HUMB17HSD	17 beta hydroxysteroid dehydro	av dif pos
L12711_s_at	HUMTRANSKE	transketolase \{tk\} mRNA, :"	av dif pos
L12711_s_at	HUMTRANSKE	transketolase \{tk\} mRNA, :"	av dif pos
L18493_s_at	HUMFMR1R	FMR1 gene, 3'end.	av dif pos
L18527_at	HUMRPL27	ribosomal protein L27 \{RPL27	av dif pos
L19686_ma1_at	HUMMIF	macrophage migration inhibitor	av dif pos
L19686_ma1_at	HUMMIF	macrophage migration inhibitor	av dif pos
L19779_at	HUMH2A2A	histone H2A.2 mRNA, :H2A hist	av dif pos
L20688_at	HUMLYGDI	GDP-dissociation inhibitor pro	av dif pos
L20941_at	HUMFERRITH	ferritin heavy chain mRNA, :f	av dif pos
L21954_at	HSPBR4	peripheral benzodiazepine rece	av dif pos
L21954_at	HSPBR4	peripheral benzodiazepine rece	av dif pos
L26247_at	HUMSUIISO	sui1 iso1 mRNA,	av dif pos
L27943_at	HUMCYDE	cytidine deaminase \{CDA\} mRN	av dif pos
L32866_at	HUMEPR1NP	effector cell protease recepto	av dif pos
L32976_at	HUMMLK3A	protein kinase \{MLK-3\} mRNA,	av dif pos
L33075_at	HUMIQGA	ras GTPase-activating-like pro	av dif pos
L33243_at	HUMPKD1A	polycystic kidney disease 1 pr	av dif pos
L33842_ma1_at	HUMIMPDH	\{clone FFE-7\} type II inosin	av dif pos
L33842_ma1_at	HUMIMPDH	\{clone FFE-7\} type II inosin	av dif pos
L33930_s_at	HUMCD24B	CD24 signal transducer mRNA, c	av dif pos
L37127_at	HUMRPIA	RNA polymerase II mRNA, :poly	av dif pos
L38490_s_at	HUMADPRF	ADP-ribosylation factor mRNA,	av dif pos
L38928_at	HUMMETSYN	5,10-methenyltetrahydrofolate	av dif pos
L38941_at	HUMRPL34A	ribosomal protein L34 \{RPL34	av dif pos
L39059_at	HUMTFSL1A	transcription factor SL1 mRNA,	av dif pos
L40357_at	HUMTRIP7M	thyroid receptor interactor \{	av dif pos
L40379_at	HUMTRIP10M	thyroid receptor interactor \{	av dif pos
L40387_at	HUMTRIP14G	thyroid receptor interactor \{	av dif pos
L40392_at	HUMORFB	\{clone S164\} mRNA, 3' end of	av dif pos
L40904_at	HUMPPARGB	H. sapiens peroxisome prolifer	av dif pos
L41870_at	HUMRB1MRNA	retinoblastoma susceptibility	av dif pos
L42176_at	HUMDRAL	\{clone 35.3\} DRAL mRNA, : \{	av dif pos
L42373_at	HUMPP2A	phosphatase 2A B56-alpha \{PP2	av dif pos
L42542_at	HUMRIP1R	RLIP76 protein mRNA, :RLIP76	av dif pos
L76159_at	HUMFRG1R	FRG1 mRNA, :FSHD region gene	av dif pos
L76465_at	HUMPGDHB	NAD+-dependent 15 hydroxyprost	av dif pos
L77886_at	HUMPTPC	protein tyrosine phosphatase m	av dif pos
M10612_at	HUMAPOCII	apolipoprotein C-II gene,	av dif pos
M11119_at	HUMERRNA	endogenous retrovirus envelope	av dif pos
M11147_at	HUMFERL	ferritin L chain mRNA, :ferr	av dif pos
M11313_s_at	HUMA2M	alpha-2-macroglobulin mRNA, :	av dif pos
M11353_at	HUMHISH3C	H3.3 histone class C mRNA,	av dif pos
M12529_at	HUMAPOE	apolipoprotein E mRNA, :apol	av dif pos
M12529_at	HUMAPOE	apolipoprotein E mRNA, :apol	av dif pos
M12886_at	HUMTCBY	T-cell receptor active beta-ch	av dif pos
M12886_at	HUMTCBY	T-cell receptor active beta-ch	av dif pos
M13207_at	HUMCSFGMA	granulocyte-macrophage colony-	av dif pos
M13560_s_at	HUMIAIG8	la-associated invariant gamma-	av dif pos
M13666_at	HUMCMYBB	c-myb mRNA, 3' end.	av dif pos
M13755_at	HUMIFN15K	interferon-induced 17-kDa/15-k	av dif pos
M13829_s_at	HUMPKS	putative raf related protein	av dif pos
M13829_s_at	HUMPKS	putative raf related protein	av dif pos

M13903_at	HUMINV2	involucrin gene, exon 2. :invo	av dif pos
M13929_s_at	HUMMYCPOA	c-myc-P64 mRNA, initiating fro	av dif pos
M13929_s_at	HUMMYCPOA	c-myc-P64 mRNA, initiating fro	av dif pos
M13934_cds2_at	HUMRPS14	ribosomal protein S14 gene, :	av dif pos
M13955_at	HUMKERMII	mesothelial keratin K7 \type	av dif pos
M14199_s_at	HUMLAMR	laminin receptor \2H5 epitope	av dif pos
M14199_s_at	HUMLAMR	laminin receptor \2H5 epitope	av dif pos
M14328_s_at	HUMENOA	alpha enolase mRNA, :enolase	av dif pos
M14483_ma1_s_at	HUMTHYMAA	prothymosin alpha mRNA,	av dif pos
M14676_at	HUMSLK	src-like kinase \sik\ mRNA,	av dif pos
M14676_at	HUMSLK	src-like kinase \sik\ mRNA,	av dif pos
M15395_at	HUMLAP	leukocyte adhesion protein \L	av dif pos
M15661_at	HUMRPZH21	ribosomal protein mRNA, :ribo	av dif pos
M15661_at	HUMRPZH21	ribosomal protein mRNA, :ribo	av dif pos
M16038_at	HUMLYN	lyn mRNA encoding a tyrosine k	av dif pos
M17733_at	HUMTHYB4	thymosin beta-4 mRNA, :thymos	av dif pos
M17863_s_at	HUMFFI2B	preproinsulin-like growth fact	av dif pos
M17863_s_at	HUMFFI2B	preproinsulin-like growth fact	av dif pos
M17885_at	HUMPPARP0	acidic ribosomal phosphoprotei	av dif pos
M17886_at	HUMPPARP1	acidic ribosomal phosphoprotei	av dif pos
M18000_at	HUMRPS17A	ribosomal protein S17 gene, :	av dif pos
M18737_ma1_at	HUMHFSP	Hanukah factor serine protease	av dif pos
M19045_f_at	HUMLSZH	lysozyme mRNA, :lysozyme ""m	av dif pos
M19159_at	HUMALPPD	placental heat-stable alkaline	av dif pos
M19159_at	HUMALPPD	placental heat-stable alkaline	av dif pos
M19301_at	HUMKAD	branched-chain alpha-keto acid	av dif pos
M19878_s_at	HUMCALB01	calbindin 27 gene, exons 1 and	av dif pos
M20902_at	HUMAPOCIA	apolipoprotein C-I \VLDL\ ge	av dif pos
M20902_at	HUMAPOCIA	apolipoprotein C-I \VLDL\ ge	av dif pos
M21142_cds2_s_at	HUMGNAS6	guanine nucleotide-binding pro	av dif pos
M21142_cds2_s_at	HUMGNAS6	guanine nucleotide-binding pro	av dif pos
M21186_at	HUMNCBLCA	neutrophil cytochrome b light	av dif pos
M21186_at	HUMNCBLCA	neutrophil cytochrome b light	av dif pos
M21302_at	HUMSPR2B	small proline rich protein \s	av dif pos
M21984_at	HUMTRT	\clone PWHTnT16\ skeletal mu	av dif pos
M22490_at	HUMBMP2B	bone morphogenetic protein-2B	av dif pos
M22960_at	HUMPPR	protective protein mRNA, :pro	av dif pos
M23178_s_at	HUMG0S19A	homologue-1 of gene encoding a	av dif pos
M23613_at	HUMNPM	nucleophosmin mRNA, :nucleoph	av dif pos
M24194_at	HUMMHBA123	MHC protein homologous to chic	av dif pos
M24194_at	HUMMHBA123	MHC protein homologous to chic	av dif pos
M24485_s_at	HUMGSTP1G	\clone pHGST-pi\ glutathione	av dif pos
M24486_s_at	HUMPYHBASA	prolyl 4-hydroxylase alpha sub	av dif pos
M25079_s_at	HUMBETGLA	sickle cell beta-globin mRNA,	av dif pos
M25079_s_at	HUMBETGLA	sickle cell beta-globin mRNA,	av dif pos
M25280_at	HUMLNHR	lymph node homing receptor mRN	av dif pos
M26311_s_at	HUMCFA	cystic fibrosis antigen mRNA,	av dif pos
M26311_s_at	HUMCFA	cystic fibrosis antigen mRNA,	av dif pos
M26665_s_at	HUMHIS2X	histatin 2 \HIS2\ mRNA, :hl	av dif pos
M26708_s_at	HUMPTAA	prothymosin alpha mRNA \ProT-	av dif pos
M26730_s_at	HUMQBPC6	mitochondrial ubiquinone-bindi	av dif pos
M27281_at	HUMVPF	vascular permeability factor m	av dif pos
M27749_r_at	HUMIGLR141	immunoglobulin-related 14.1 pr	av dif pos
M27749_r_at	HUMIGLR141	immunoglobulin-related 14.1 pr	av dif pos
M27826_at	HUMRTVLH3	endogenous retroviral protease	av dif pos

M27891_at	HUMCYS3A3	cystatin C (CST3) gene, exon	av dif pos
M28212_at	HUMRAB6A	GTP-binding protein (RAB6) m	av dif pos
M28882_s_at	HUMMUC18B	MUC18 glycoprotein mRNA, :mel	av dif pos
M28882_s_at	HUMMUC18B	MUC18 glycoprotein mRNA, :mel	av dif pos
M29335_at	HUMMHDOA	MHC class II DO-alpha mRNA,	av dif pos
M29335_at	HUMMHDOA	MHC class II DO-alpha mRNA,	av dif pos
M29610_s_at	HUMGLYE	glycophorin E mRNA, :glycopho	av dif pos
M30818_at	HUMMXB	interferon-induced cellular re	av dif pos
M30938_at	HUMKUP	Ku (p70/p80) subunit mRNA,	av dif pos
M31303_ma1_at	HUMOP18A	oncoprotein 18 (Op18) gene,	av dif pos
M31303_ma1_at	HUMOP18A	oncoprotein 18 (Op18) gene,	av dif pos
M31520_at	HUMRPS24A	ribosomal protein S24 mRNA,	av dif pos
M31520_ma1_s_at	HUMRPS24A	ribosomal protein S24 mRNA, :r	av dif pos
M31627_at	HUMHXPB1	X box binding protein-1 (XBP-	av dif pos
M31994_at	HUMALDC13	aldehyde dehydrogenase (ALDH1	av dif pos
M32053_at	HUMH19	H19 RNA gene,	av dif pos
M32304_s_at	HUMMET	metalloproteinase inhibitor mR	av dif pos
M32405_at	HUMRIGA	homologue of rat insulinoma ge	av dif pos
M32886_at	HUMSRICPA	sorcin CP-22 mRNA, :sorcin :s	av dif pos
M33600_f_at	HUMMHDR1C	MHC class II HLA-DR-beta-1 (H	av dif pos
M33680_at	HUMTAPA1	28-kDa cell surface protein TA	av dif pos
M33684_s_at	HUMPPP1A5	(clone lambda-16-1) non-rece	av dif pos
M34041_at	HUMADRA2RA	alpha-2-adrenergic receptor (av dif pos
M34182_at	HUMPRKACG	testis-specific protein kinase	av dif pos
M34516_at	HUMIGL122	omega light chain protein 14.1	av dif pos
M34516_r_at	HUMIGL122	omega light chain protein 14.1	av dif pos
M34516_r_at	HUMIGL122	omega light chain protein 14.1	av dif pos
M34715_at	HUMPSBGAA	pregnancy-specific beta-1-glyc	av dif pos
M34996_s_at	HUMDQA1A	MHC cell surface glycoprotein	av dif pos
M34996_s_at	HUMDQA1A	MHC cell surface glycoprotein	av dif pos
M35198_at	HUMINTB6A	integrin B-6 mRNA, :integrin,	av dif pos
M35252_at	HUMCOOTAA	CO-029, :transmembrane 4 super	av dif pos
M35878_at	HUMIBP3	insulin-like growth factor-bin	av dif pos
M36072_at	HUMRPL7A	ribosomal protein L7a (surf 3	av dif pos
M37238_s_at	HUMPLC	phospholipase C mRNA, :phosph	av dif pos
M37245_at	HUMIGCTL3	Ig superfamily cytotoxic T-lym	av dif pos
M37245_at	HUMIGCTL3	Ig superfamily cytotoxic T-lym	av dif pos
M37435_at	HUMCSDF1	macrophage-specific colony-sti	av dif pos
M37583_at	HUMHIS2AZ	histone (H2A.Z) mRNA, :hist	av dif pos
M37815_cds1_at	HUMCD284	T-cell membrane glycoprotein C	av dif pos
M38449_s_at	HUMTGFB	transforming growth factor-bet	av dif pos
M38690_at	HUMANTCD9	CD9 antigen mRNA, :CD9 antige	av dif pos
M38690_at	HUMANTCD9	CD9 antigen mRNA, :CD9 antige	av dif pos
M54995_at	HUMCTAP3	connective tissue activation p	av dif pos
M55409_s_at	HUMPANCAN	pancreatic tumor-related prote	av dif pos
M55409_s_at	HUMPANCAN	pancreatic tumor-related prote	av dif pos
M57293_at	HUMPTHSPA	parathyroid hormone-related pe	av dif pos
M57399_at	HUMHBNF1	nerve growth factor (HBNF-1)	av dif pos
M57399_at	HUMHBNF1	nerve growth factor (HBNF-1)	av dif pos
M57466_s_at	HUMMHDPL	MHC class II HLA-DP light chai	av dif pos
M57466_s_at	HUMMHDPL	MHC class II HLA-DP light chai	av dif pos
M57710_at	HUMBPIGE	IgE-binding protein (epsilon-	av dif pos
M58378_cds1_at	HUMSYN1E13	synapsin I (SYN1) gene, exon	av dif pos
M58525_s_at	HUMCOMTC	catechol-O-methyltransferase	av dif pos
M58525_s_at	HUMCOMTC	catechol-O-methyltransferase	av dif pos

M59216_s_at	UMGABRB1S5	gamma-aminobutyric acid-A (GA	av dif pos
M59371_at	HUMECK	protein tyrosine kinase mRNA,	av dif pos
M59807_at	HUMNK4	NK4 mRNA, :natural killer cel	av dif pos
M59830_at	HUMMHSP2	MHC class III HSP70-2 gene (H	av dif pos
M59911_at	HUMINTA3A	integrin alpha-3 chain mRNA,	av dif pos
M60483_ma1_s_at	HUMPP2AA	protein phosphatase 2A catalyt	av dif pos
M60854_at	HUMSRAA	ribosomal protein S16 mRNA, :	av dif pos
M61916_at	HUMLAM101	laminin B1 chain mRNA, :lamin	av dif pos
M62403_s_at	HUMIGFBP5	insulin-like growth factor bin	av dif pos
M62403_s_at	HUMIGFBP5	insulin-like growth factor bin	av dif pos
M62486_at	UMPRPC4S12	C4b-binding protein gene, exon	av dif pos
M63256_at	HUMCDR2AA	major Yo paraneoplastic antige	av dif pos
M63379_at	HUMTRPM2A4	TRPM-2 protein gene, exons 7,8	av dif pos
M63438_s_at	HUMIGGK	Ig rearranged gamma chain mRNA	av dif pos
M63438_s_at	HUMIGGK	Ig rearranged gamma chain mRNA	av dif pos
M63573_at	HUMSCYLP	secreted cyclophilin-like prot	av dif pos
M63589_at	HUMSCL7	stem cell leukemia gene produc	log neg
M64347_at	HUMFGFLR	novel growth factor receptor m	log neg
M64347_at	HUMFGFLR	novel growth factor receptor m	log neg
M64673_at	HUMHSF1	heat shock factor 1 (TCF5) m	log neg
M64716_at	HUMRPS25	ribosomal protein S25 mRNA, :	log neg
M64992_at	HUMPROS30	prosome protein P30-33K (pro	log neg
M65292_s_at	HUMHAAA	factor H homologue mRNA, :fa	log neg
M65292_s_at	HUMHAAA	factor H homologue mRNA, :fa	log neg
M69023_at	HUMGGEFERA	globin gene.	log neg
M69066_at	HUMMOESIN	moesin mRNA, :moesin :moesin	log neg
M69238_at	HUMARNTA	aryl hydrocarbon receptor nucl	log neg
M73077_at	HUMGRF1A	glucocorticoid receptor repres	log neg
M73239_s_at	HUMSCFA1	(clone SF1) hepatocyte growt	log neg
M73547_at	HUMPOLLA	polyposis locus (DP1 gene) m	log neg
M74093_at	HUMCLNC	cyclin mRNA. :cyclin E1	log neg
M74297_at	HUMHOX14	homeobox 1.4 protein mRNA, :h	log neg
M74715_s_at	HUMIDNAL	alpha-L-iduronidase (IDUA) mR	log neg
M77232_ma1_at	HUMRPS6B	ribosomal protein S6 gene, com	log neg
M77836_at	HUMP5CR	pyrroline 5-carboxylate reduct	log neg
M80244_at	HUME16GEN	E16 mRNA,	log neg
M80254_at	HUMCYP	cyclophilin isoform (hCyp3)	log neg
M80359_at	HUMP78A	protein p78 mRNA, :MAP/microt	log neg
M80563_at	HUMCAPL	CAPL protein mRNA, :S100 calc	log neg
M80563_at	HUMCAPL	CAPL protein mRNA, :S100 calc	log neg
M80899_at	HUMAHPNAKA	novel protein AHPNAK mRNA, part	log neg
M81750_at	HUMMCNDA	myeloid cell nuclear different	log neg
M81757_at	HUMS19RP	S19 ribosomal protein mRNA,	log neg
M81883_at	HUMGAD67A	glutamate decarboxylase (GAD6	log neg
M83181_at	HUMHTRB	serotonin receptor gene, :5-h	log neg
M84424_at	HUMCTSE09	cathepsin E (CTSE) gene, exo	log neg
M84711_at	HUMFTE1A	v-fos transformation effector	log neg
M85289_at	HUMHSPG2B	heparan sulfate proteoglycan	log neg
M86400_at	HUMPHPLA2	phospholipase A2 mRNA, :tyros	log neg
M86699_at	HUMTTK	kinase (TTK) mRNA, :TTK pro	log neg
M86737_at	HUMHMGBP	high mobility group box (SSRP	log neg
M87789_s_at	HUMIGHEPAH	(hybridoma H210) anti-hepati	log neg
M87789_s_at	HUMIGHEPAH	(hybridoma H210) anti-hepati	log neg
M90356_f_at	HUMBTFD	BTF3 protein homologue gene,	log neg
M90656_at	HUMGCSH	gamma-glutamylcysteine synthet	log neg

M91670_at	HUME2EP1	ubiquitin carrier protein \E2	log neg
M94856_at	HUMFABPHA	fatty acid binding protein hom	log neg
M94856_at	HUMFABPHA	fatty acid binding protein hom	log neg
M94880_f_at	HUMHLAAX	MHC class I \HLA-A*8001\ mRNA	log neg
M96233_s_at	HUMGSTM4A	glutathione transferase class	log neg
M96233_s_at	HUMGSTM4A	glutathione transferase class	log neg
M96326_ma1_at	HUMAZCDI	azurocidin gene,	log neg
M96956_at	HUMTDGF3A	\clone CR-3\ teratocarcinoma	log neg
M97796_s_at	HUMID2X	helix-loop-helix protein \Id-	log neg
M97815_at	HUMCRABP02	retinoic acid-binding protein	log neg
S34389_at	HMOX2	heme oxygenase-2 [human, kidney]	log neg
S58544_at	SPAG1	75 kDa infertility-related spe	log neg
S69115_at	S69115	granulocyte colony-stimulating	log neg
S69115_at	S69115	granulocyte colony-stimulating	log neg
S71043_ma1_s_at	S71043	Ig alpha 2=immunoglobulin A he	log neg
S71043_ma1_s_at	S71043	Ig alpha 2=immunoglobulin A he	log neg
S73591_at	VDUP1	brain-expressed HHCPA78 homolo	log neg
S73591_at	VDUP1	brain-expressed HHCPA78 homolo	log neg
S75463_at	S75463	P43=mitochondrial elongation f	log neg
S77356_at	S77356	transcript ch21=oligomycin sen	log neg
S77582_at	S77582	HERVK10/HUMMTV reverse transcr	log neg
S78234_at	S78234	nuc2 homolog [human, fibroblas	log neg
S78771_s_at	S78771	NAT=CpG island-associated gene	log neg
S79219_s_at	S79219	metastasis-associated gene [hu	log neg
S79522_at	S79522	ubiquitin carboxyl extension p	log neg
S80562_at	CNN3	acidic calponin [human, kidney]	log neg
S82297_at	S82297	beta 2-microglobulin {11bp del	log neg
S82597_ma1_s_at	S82597	UDP-GalNAc:polypeptide	log neg
S90469_at	POR	cytochrome P450 reductase [hum	log neg
U00947_s_at	U00947	clone C4E 3.2 \CAC\ n\GTG\	log neg
U03397_s_at	U03397	receptor protein 4-1BB mRNA,	log neg
U03398_at	TNFSF9	receptor 4-1BB ligand mRNA, :	log neg
U04241_at	U04241	homolog of Drosophila enhancer	log neg
U04313_at	PI5	maspin mRNA, :protease inhibi	log neg
U05340_at	CDC20	p55CDC mRNA, :cell division c	log neg
U06155_s_at	U06155	chromosome 1q subtelomeric seq	log neg
U06863_at	U06863	folliculin-related protein pr	log neg
U06863_at	U06863	folliculin-related protein pr	log neg
U09117_at	PLCD1	phospholipase C delta 1 mRNA,	log neg
U09303_at	EFNB1	T cell leukemia LERK-2 \EPLG2	log neg
U09813_at	ATP5G3	mitochondrial ATP synthase sub	log neg
U09953_at	U09953	ribosomal protein L9 mRNA, :r	log neg
U10362_at	U10362	GP36b glycoprotein mRNA,	log neg
U10492_at	HSMOX1	Mox1 protein \MOX1\ mRNA, :	log neg
U12404_at	U12404	Csa-19 mRNA,	log neg
U12404_at	U12404	Csa-19 mRNA,	log neg
U12465_at	U12465	ribosomal protein L35 mRNA,	log neg
U12779_at	U12779	MAP kinase activated protein k	log neg
U14391_at	MYO1C	myosin-IC mRNA, :myosin IC	log neg
U14588_at	PXN	paxillin mRNA, :paxillin :pax	log neg
U14968_at	U14968	ribosomal protein L27a mRNA,	log neg
U14969_at	U14969	ribosomal protein L28 mRNA, :	log neg
U14970_at	U14970	ribosomal protein S5 mRNA, :r	log neg
U14971_at	U14971	ribosomal protein S9 mRNA, :r	log neg
U14971_at	U14971	ribosomal protein S9 mRNA, :r	log neg

U14972_at	U14972	ribosomal protein S10 mRNA,	log neg
U14973_at	U14973	ribosomal protein S29 mRNA, :	log neg
U15177_at	U15177	cosmid CRI-JC2015 at D10S289 I	log neg
U16860_at	ECH1	peroxisomal enoyl-CoA hydratase	log neg
U16799_s_at	U16799	Na,K-ATPase beta-1 subunit mRNA	log neg
U16861_at	KCNJ2	inward rectifying potassium ch	log neg
U17077_at	BENE	BENE mRNA, :BENE protein	log neg
U17760_ma1_at	HSLAMB3S17	laminin S B3 chain \(\Lambda MB3\)	log neg
U19247_ma1_s_at	HSINFGRA7	interferon-gamma receptor alph	log neg
U19251_s_at	NAIP	neuronal apoptosis inhibitory	log neg
U20657_at	USP4	ubiquitin protease \(\text{Unph}\)	log neg
U20734_s_at	U20734	transcription factor junB \(\text{ju}\)	log neg
U20734_s_at	U20734	transcription factor junB \(\text{ju}\)	log neg
U20758_ma1_at	U20758	osteopontin gene,	log neg
U22376_cds2_s_at	MYB	\(\text{c-myb}\)	log neg
U22431_s_at	U22431	hypoxia-inducible factor 1 alp	log neg
U22970_ma1_s_at	U22970	interferon-inducible peptide	log neg
U22970_ma1_s_at	U22970	interferon-inducible peptide	log neg
U24183_s_at	U24183	phosphofructokinase \(\text{PFKM}\)	log neg
U24389_s_at	HSLYOXL7	lysyl oxidase-like protein gen	log neg
U25789_at	U25789	ribosomal protein L21 mRNA, :	log neg
U27333_at	U27333	alpha \(\text{1,3}\)	log neg
U27333_at	U27333	alpha \(\text{1,3}\)	log neg
U27831_at	U27831	striatum-enriched phosphatase	log neg
U29175_at	U29175	transcriptional activator \(\text{BR}\)	log neg
U29953_ma1_at	PEDF	pigment epithelium-derived fac	log neg
U30827_s_at	U30827	splicing factor SRp40-3 \(\text{SRp4}\)	log neg
U30888_at	USP14	tRNA-guanine transglycosylase	log neg
U30888_at	USP14	tRNA-guanine transglycosylase	log neg
U31814_at	HDAC2	transcriptional regulator homo	log neg
U31875_at	HEP27	Hep27 protein mRNA, :short-ch	log neg
U32944_at	PIN	cytoplasmic dynein light chain	log neg
U34880_at	U34880	DPH2L mRNA, :DPH2L "mRNA," co	log neg
U36341_ma1_at	U36341	Xq28 cosmid, creatine transpor	log neg
U36764_at	U36764	TGF-beta receptor interacting	log neg
U37012_at	U37012	cleavage and polyadenylation s	log neg
U37146_at	U37146	silencing mediator of retinoid	log neg
U37408_at	CTBP1	phosphoprotein CtBP mRNA, :C-	log neg
U37689_at	POLR2H	RNA polymerase II subunit \(\text{hs}\)	log neg
U38276_at	SEMA3F	semaphorin III family homolog	log neg
U38276_at	SEMA3F	semaphorin III family homolog	log neg
U39400_at	C11orf4	NOF1 mRNA, :chromosome 11 op	log neg
U40998_at	U40998	retinal protein \(\text{HRG4}\)	log neg
U41060_at	U41060	breast cancer, estrogen regula	log neg
U41766_s_at	ADAM9	metalloprotease/disintegrin/cy	log neg
U42359_at	HUMN33S10	N33 protein form 1 \(\text{N33}\)	log neg
U43328_at	U43328	link protein mRNA,	log neg
U43901_ma1_s_at	U43901	37 kD laminin receptor precurs	log neg
U43901_ma1_s_at	U43901	37 kD laminin receptor precurs	log neg
U45448_s_at	U45448	P2x1 receptor mRNA,	log neg
U48705_ma1_s_at	U48705	receptor tyrosine kinase DDR g	log neg
U48936_at	U48936	amiloride-sensitive epithelial	log neg
U48936_at	U48936	amiloride-sensitive epithelial	log neg
U49395_at	U49395	ionotropic ATP receptor P2X5a	log neg
U49869_ma1_at	UBB	ubiquitin gene, :ubiquitin B	log neg

U50523_at	U50523	BRCA2 region, mRNA sequence CG	log neg
U50829_at	BHMT	betaine:homocysteine methyltra	log neg
U52154_at	KCNJ5	G protein-coupled inwardly rec	log neg
U52154_at	KCNJ5	G protein-coupled inwardly rec	log neg
U52696_s_at	U52696	adrenal Creb-rp homolog \{Creb	log neg
U53786_at	U53786	envoplakin \{EVPL\} mRNA, :en	log neg
U55054_at	HSKCC	K-Cl cotransporter \{hKCC1\} m	log neg
U55054_at	HSKCC	K-Cl cotransporter \{hKCC1\} m	log neg
U57341_r_at	U57341	neurofilament triplet L protei	log neg
U57342_at	MLF2	myelodysplasia/myeloid leukemi	log neg
U57629_at	RPGR	retinitis pigmentosa GTPase re	log neg
U58682_at	U58682	ribosomal protein S28 mRNA, :	log neg
U60975_at	U60975	hybrid receptor gp250 precurs	log neg
U60975_at	U60975	hybrid receptor gp250 precurs	log neg
U62739_at	BCAT2	branched-chain amino acid amin	log neg
U62962_at	EIF3S6	Int-6 mRNA, :eukaryotic trans	log neg
U63541_at	U63541	mRNA expressed in HC/HCC liver	log neg
U64863_at	PDCD1	hPD-1 \{hPD-1\} mRNA, :progra	log neg
U66061_cds3_at	U66061	germline T-cell receptor beta	log neg
U66406_at	EFNB3	putative EPH-related PTK recep	log neg
U66616_at	SMARCC2	SWI/SNF complex 170 KDa subuni	log neg
U66616_at	SMARCC2	SWI/SNF complex 170 KDa subuni	log neg
U67092_s_at	U67092	ataxia-telangiectasia locus pr	log neg
U67156_at	MEKK5	mitogen-activated kinase kinas	log neg
U68105_s_at	HSPABPS13	poly\{A\}-binding protein \{PA	log neg
U70732_ma1_at	GPT	glutamate pyruvate transaminas	log neg
U70867_at	SLC21A2	prostaglandin transporter hPGT	log neg
U73379_at	U73379	cyclin-selective ubiquitin car	log neg
U73379_at	U73379	cyclin-selective ubiquitin car	log neg
U73824_at	EIF4G2	p97 mRNA, :eukaryotic transla	log neg
U73843_at	U73843	epithelial-specific transcript	log neg
U77456_at	NAP1L4	nucleosome assembly protein 2	log neg
U77846_ma1_at	U77846	elastin gene, partial cds and	log neg
U77846_ma1_s_at	U77846	elastin gene, partial cds and	log neg
U77846_ma1_s_at	U77846	elastin gene, partial cds and	log neg
U78027_ma3_at	U78027	Bruton's tyrosine kinase \{BTK	log neg
U78095_at	U78095	placental bikunin mRNA, :Plac	log neg
U78678_at	U78678	thioredoxin mRNA, nuclear gene	log neg
U78722_at	U78722	zinc finger protein 165 \{Zpf1	log neg
U78735_at	U78735	ABC3 mRNA,	log neg
U79256_at	U79256	clone 23719 mRNA sequence.	log neg
U79280_at	U79280	clone 23575 mRNA,	log neg
U79299_at	U79299	neuronal olfactomedin-related	log neg
U80184_ma1_at	FLII	FLII gene, :flightless I \{Dr	log neg
U81984_at	EPAS1	endothelial PAS domain protein	log neg
U82169_at	FZD9	frizzled homolog \{FZD3\} mRNA	log neg
U82169_at	FZD9	frizzled homolog \{FZD3\} mRNA	log neg
U82818_at	U82818	UCP3S mRNA,	log neg
U83246_at	CPNE1	copine I mRNA, :copine I :cop	log neg
U83598_at	U83598	death domain receptor 3 solubl	log neg
U86136_at	U86136	telomerase-associated protein	log neg
U87972_at	U87972	NAD+-isocitrate dehydrogenase	log pos
U88964_at	ISG20	HEM45 mRNA, :interferon stimu	log pos
U89326_at	U89326	bone morphogenetic protein rec	log pos
U90426_at	DDXL	nuclear RNA helicase, :nuclea	log pos

U90552_s_at	U90552	butyrophilin (BTF5) mRNA, :	log pos
U90913_at	U90913	clone 23665 mRNA sequence. :cl	log pos
U90916_at	U90916	clone 23815 mRNA sequence. :cl	log pos
U94747_at	HAN11	WD repeat protein HAN11 mRNA,	log pos
U95740_ma1_at	U95740	Chromosome 16 BAC clone CIT987	log pos
V00571_ma1_at	HSPCRF	gene encoding prepro form of c	log pos
V00572_at	HSPGK1	mRNA encoding phosphoglycerate	log pos
V00594_s_at	HSTHIO	metallothionein from cadmium-	log pos
V01512_ma1_at	HSCFOS	cellular oncogene c-fos (comp	log pos
X00274_at	HSHL07	gene for HLA-DR alpha heavy ch	log pos
X00274_at	HSHL07	gene for HLA-DR alpha heavy ch	log pos
X00351_f_at	HSAC07	beta-actin.	log pos
X00368_xpt2_at	HSPROL1	prolactin gene 5' region.	log pos
X01677_f_at	HSGAPDR	liver glyceraldehyde-3-phosph	log pos
X02152_at	HSLDHAR	lactate dehydrogenase-A (LDH	log pos
X02596_at	HSBCRR	bcr (breakpoint cluster regi	log pos
X03068_f_at	HSHLDQWB	HLA-D class II antigen DQw1.1	log pos
X03100_cds2_at	HSHLASBA	HLA-SB(DP) alpha gene. :HLA-	log pos
X03100_cds2_at	HSHLASBA	HLA-SB(DP) alpha gene. :HLA-	log pos
X03342_at	HSRPL32	ribosomal protein L32. :ribos	log pos
X03689_s_at	HSEFTUR5	mRNA fragment for elongation f	log pos
X03689_s_at	HSEFTUR5	mRNA fragment for elongation f	log pos
X04347_s_at	HSUPIR1	liver mRNA fragment DNA bindin	log pos
X04347_s_at	HSUPIR1	liver mRNA fragment DNA bindin	log pos
X06614_at	HSRRA	receptor of retinoic acid. :r	log pos
X06617_at	HSRPS11	ribosomal protein S11. :ribo	log pos
X06985_at	HSOXYGR	heme oxygenase. :heme oxygena	log pos
X06985_at	HSOXYGR	heme oxygenase. :heme oxygena	log pos
X07696_at	HSKERC15	cytokeratin 15. :keratin 15 :	log pos
X07730_at	HSPSA	prostate specific antigen. :	log pos
X07730_at	HSPSA	prostate specific antigen. :	log pos
X12447_at	HSALDOA	aldolase A gene (EC 4.1.2.13	log pos
X12671_ma1_at	HSHNRNPA	gene for heterogeneous nuclear	log pos
X12671_ma1_at	HSHNRNPA	gene for heterogeneous nuclear	log pos
X12876_s_at	HSKER18A	mRNA fragment for cytokeratin	log pos
X12876_s_at	HSKER18A	mRNA fragment for cytokeratin	log pos
X13334_at	HSCD14R	CD14 myeloid cell-specific leu	log pos
X13546_ma1_at	HSHMG17G	HMG-17 gene for non-histone ch	log pos
X13794_ma1_at	HSLDHB1	lactate dehydrogenase B gene e	log pos
X13794_ma1_at	HSLDHB1	lactate dehydrogenase B gene e	log pos
X14008_ma1_f_at	HSLYSOZY	lysozyme gene (EC 3.2.1.17).	log pos
X15940_at	HSRPL31	ribosomal protein L31. :ribos	log pos
X16064_at	HSTUMP	translationally controlled tu	log pos
X16832_at	HSCATHH	cathepsin H (EC 3.4.22.16).	log pos
X17042_at	HSHPCP	hematopoietic proteoglycan cor	log pos
X17206_at	HSLREP3	LLRep3. : LLRep3	log pos
X51345_at	HSJUNB	jun-B JUN-B protein. :jun B p	log pos
X51466_at	HSEF2	elongation factor 2. : elonga	log pos
X51688_at	HSCYCLINA	cyclin A.	log pos
X52003_at	HSPS2MKN	pS2 protein gene. :trefoil fac	log pos
X52003_at	HSPS2MKN	pS2 protein gene. :trefoil fac	log pos
X52426_s_at	HSCYTK	cytokeratin 13. : cytokeratin	log pos
X52426_s_at	HSCYTK	cytokeratin 13. : cytokeratin	log pos
X52851_ma1_at	HSCPH70	cyclophilin gene for cyclophil	log pos
X52966_at	HSL35A	ribosomal protein L35a. :ribo	log pos

X53586_ma1_at	HSINTA8R	integrin alpha 6. :integrin,	log pos
X53587_at	HSINTB4R	integrin beta 4. : integrin b	log pos
X53777_at	HSL23MR	L23 putative ribosomal protel	log pos
X54232_at	HSGLYPIC	heparan sulfate proteoglycan	log pos
X54667_at	HSCYSTATS	cystatin S.	log pos
X54942_at	HSCKSHS2	ckshs2 Cks1 protein homologue	log pos
X54942_at	HSCKSHS2	ckshs2 Cks1 protein homologue	log pos
X55005_ma1_at	HSCERBAR	c-erbA-1 thyroid hormone rece	log pos
X55715_at	HSUMS3	Hums3 40S ribosomal protein s	log pos
X55954_at	HSL17ARP	HL23 ribosomal protein homolo	log pos
X56494_at	HSPKM12	M gene for M1-type and M2-type	log pos
X56687_s_at	HSAUTNOR	autoantigen NOR-90.	log pos
X56807_at	HSDGII	DSC2 desmocollins type 2a and	log pos
X56841_at	HSHLAE	HLA-E gene. :major histocompat	log pos
X56932_at	HS23KDHP	23 kD highly basic protein.	log pos
X57351_at	HS18D	1-8D gene from interferon-indu	log pos
X57351_at	HS18D	1-8D gene from interferon-indu	log pos
X57351_s_at	HS18D	1-8D gene from interferon-indu.	log pos
X57809_s_at	HSIGVL009	rearranged immunoglobulin lamb	log pos
X57809_s_at	HSIGVL009	rearranged immunoglobulin lamb	log pos
X57959_at	HSRBPRL7A	ribosomal protein L7. :riboso	log pos
X58072_at	HSGATA3R	hGATA3 trans-acting T-cell sp	log pos
X59373_at	HSHOX4D	HOX4D a homeobox protein. :ho	log pos
X59798_at	HSPRAD1CY	PRAD1 cyclin. :PRAD1 cyclin	log pos
X60489_at	HSEF1B	elongation factor-1-beta.	log pos
X61587_at	HSRHOG	rhoG GTPase. :ras homolog gen	log pos
X62320_at	HSEPIT1	epithelin 1 and 2. : epitheli	log pos
X62466_at	HSCAMPAT1	CAMPATH-1 \ (CDw52) antigen.	log pos
X62466_at	HSCAMPAT1	CAMPATH-1 \ (CDw52) antigen.	log pos
X62654_ma1_at	HSMECDAG	gene for Me491/CD63 antigen. :	log pos
X62691_at	HSRPRNA	ribosomal protein \ (homologuo	log pos
X63359_at	HSUGT2BIO	UGT2BIO udp glucuronosyltrans	log pos
X63527_at	HSRPL19	ribosomal protein L19. :ribos	log pos
X63629_at	HSPCAD	p cadherin. :cadherin 3, P-ca	log pos
X64229_at	HSDEK9	dek mRNA. :DEK gene	log pos
X64707_at	HSBBC1	BBC1 mRNA.	log pos
X65614_at	HSS100PCB	calcium-binding protein S100P	log pos
X66114_ma1_at	HS2OXOC	gene for 2-oxoglutarate carrie	log pos
X66363_at	HSSTHPKD	mRNA PCTAIRE-1 for serine/thre	log pos
X66363_at	HSSTHPKD	mRNA PCTAIRE-1 for serine/thre	log pos
X66699_at	HSEWS	EWS mRNA. :Ewing sarcoma break	log pos
X67247_ma1_at	HSRPS8	rpS8 gene for ribosomal protel	log pos
X67325_at	HSP27	p27 mRNA. :interferon, alpha-i	log pos
X67951_at	HSPAG	proliferation-associated gene	log pos
X68314_at	HSQPGI	glutathione peroxidase-GI. :g	log pos
X68314_at	HSQPGI	glutathione peroxidase-GI. :g	log pos
X68688_ma1_s_at	HSZNB	ZNF33B gene.	log pos
X69150_at	HSRPS18	ribosomal protein S18. :ribos	log pos
X69391_at	HSRPL8AA	ribosomal protein L8. :riboso	log pos
X69550_at	HSRHO1	rho GDP-dissociation inhibito	log pos
X69654_at	HSS26	ribosomal protein S26.	log pos
X70940_s_at	HSEFAC1A2	elongation factor 1 alpha-2.	log pos
X70940_s_at	HSEFAC1A2	elongation factor 1 alpha-2.	log pos
X73079_at	HSPIR	encoding Polymeric immunoglobu	log pos
X73358_s_at	HSAES1	hAES-1 mRNA. :amino-terminal e	log pos

X73460_at	HSRPL3A	ribosomal protein L3.	log pos
X73478_at	HSPTPAA	hPTPA mRNA. :hPTPA mRNA	log pos
X74819_at	HSCARTROT	cardiac troponin T.	log pos
X74819_at	HSCARTROT	cardiac troponin T.	log pos
X74929_s_at	HSKRT8	KRT8 keratin 8. :keratin 8 :K	log pos
X75252_at	HSPEABP	phosphatidylethanolamine bindi	log pos
X76534_at	HSNMB	NMB mRNA. :transmembrane glyco	log pos
X76534_at	HSNMB	NMB mRNA. :transmembrane glyco	log pos
X77794_at	HSCYCG1	cyclin G1. : cyclin G1	log pos
X78992_at	HSERF2	ERF-2 mRNA.	log pos
X79234_at	HSRPL11	ribosomal protein L11.	log pos
X79439_at	HSNOTCH3	Notch 3 DNA sequence. :Notch	log pos
X80062_at	HSSAMRNA	SA mRNA.	log pos
X80198_at	HSMLN64	MLN64 mRNA.	log pos
X80200_at	HSMLN62	MLN62 mRNA. :TNF receptor-asso	log pos
X80822_at	HSPLORF	ORF.	log pos
X80909_at	HSANAC	alpha NAC mRNA. :nascent-polyp	log pos
X82693_at	HSE48	E48 antigen. : E48 antigen	log pos
X82693_at	HSE48	E48 antigen. : E48 antigen	log pos
X83416_s_at	HSPRP2	PrP gene, exon 2. :PrP ""gene	log pos
X83492_at	HSFAS47	Fas/Apo-1 \clone pCRTM11-Fas	log pos
X83492_at	HSFAS47	Fas/Apo-1 \clone pCRTM11-Fas	log pos
X83572_at	HSARSD	ARSD gene, complete CDS. :aryl	log pos
X86809_at	HSPEA15	major astrocytic phosphoprote	log pos
X87159_at	HSSCNN1B	beta subunit of epithelial am	log pos
X87241_at	HSHFATPRO	hFat protein. :FAT tumor supp	log pos
X89416_at	HSRNAPPP5	protein phosphatase 5. :prote	log pos
X89416_at	HSRNAPPP5	protein phosphatase 5. :prote	log pos
X90846_at	HARNAMLK2	mixed lineage kinase 2.	log pos
X91103_at	HSRNAHR44	Hr44 protein.	log pos
X93036_at	HSMAT82	MAT8 protein. :phospholemman-	log pos
X94583_xp12_r_at	HSDBIEX12	dbl/acbp gene exon 1 & 2.	log pos
X94612_at	HS2CGMPPK	type II cGMP-dependent protei	log pos
X95404_at	HSNMCFL1	non-muscle type cofilin. :cof	log pos
X95735_at	HSZYXIN2R	zyxin. :zyxin	log pos
X95808_s_at	HSDXS	protein encoded by a candidat	log pos
X98482_at	HSTNNTX11	TNNT2 gene exon 11.	log pos
X98482_r_at	HSTNNTX11	TNNT2 gene exon 11.	log pos
X98482_r_at	HSTNNTX11	TNNT2 gene exon 11.	log pos
X98534_s_at	HSVASP413	VASP gene, exons 4 to 13. :""VA	log pos
X99133_at	HSNGALGEN	NGAL gene. :lipocalin 2 \onco	log pos
X99888_at	HSTYL	mRNA from TYL gene. :pleckstrl	log pos
Y00062_at	HSLCA	T200 leukocyte common antigen	log pos
Y00503_at	HSKER19	keratin 19. :keratin 19 : ker	log pos
Y00705_at	HSPSTI	pstl pancreatic secretory inh	log pos
Y00787_s_at	HSMDNCF	MDNCF \monocyte-derived neut	log pos
Y00787_s_at	HSMDNCF	MDNCF \monocyte-derived neut	log pos
Y00796_at	HSFLA1A	leukocyte-associated molecule	log pos
Y07755_at	HSS100A2	S100A2 gene, exon 1, 2 and 3.	log pos
Y07755_at	HSS100A2	S100A2 gene, exon 1, 2 and 3.	log pos
Y08374_ma1_at	Y08374	gene encoding cartilage GP-39	log pos
Y08639_at	HSTFAC	nuclear orphan receptor ROR-b	log pos
Y08976_at	HSRNAFEV	FEV protein.	log pos
Y10207_at	HSCD171	CD171 protein.	log pos
Y10871_at	HSTWISTGE	twist gene. :twist \Drosophil	log pos

Y12670_at	HSOBRGRP	leptin receptor gene-related	log pos
Z12962_at	HSRPL41	homologue to yeast ribosomal	log pos
Z19554_s_at	HSVIMENTA	vimentin gene. :vimentin gene	log pos
Z19574_ma1_at	HSCYTOK17	gene for cytokeratin 17. :gene	log pos
Z22551_at	HSKINEC	kinectin gene.	log pos
Z25749_ma1_at	HSRPS7	gene for ribosomal protein S7.	log pos
Z25884_at	HSCLC1MR	CIC-1 muscle chloride channel	log pos
Z25884_at	HSCLC1MR	CIC-1 muscle chloride channel	log pos
Z28491_s_at	HSCOMT2	gene for catechol O-methyltran	log pos
Z28407_at	HSRBPL8	ribosomal protein L8. :riboso	log pos
Z28407_at	HSRBPL8	ribosomal protein L8. :riboso	log pos
Z30643_at	HSCLCHPRA	chloride channel \ (putative)	log pos
Z32765_at	HSCD38G15	CD38 gene exon 15.	log pos
Z35402_ma1_s_at	HSECAD3	gene encoding E-cadherin, exon	log pos
Z35402_ma1_s_at	HSECAD3	gene encoding E-cadherin, exon	log pos
Z48501_s_at	HSPABPII	polyadenylate binding protein	log pos
Z48950_at	HSHH3X3B	hH3.3B gene for histone H3.3.	log pos
Z49107_s_at	Z49107	galectin.	log pos
Z49148_s_at	HSRPL29	ribosomal protein L29.	log pos
Z49148_s_at	HSRPL29	ribosomal protein L29.	log pos
Z49835_s_at	HSP2SISOM	protein disulfide isomerase.	log pos
Z50022_at	HSSGP1N15	surface glycoprotein. :chromo	log pos
Z69043_s_at	HSTRAPRNA	mRNA translocon-associated pro	log pos
Z70759_at	HSM243	mitochondrial 16S rRNA gene \ (log pos
Z80783_at	HSH2BL	H2B/1 gene. :H2B histone famil	log pos
Z80787_at	HSH4J	H4/j gene. :H4 histone family,	log pos
Z80787_at	HSH4J	H4/j gene. :H4 histone family,	log pos
Z83804_at	HSHDHC7	axonemal dynein heavy chain	log pos
Z84721_cds2_at	HSGG1	DNA sequence from cosmid GG1 f	log pos
Z84721_cds2_at	HSGG1	DNA sequence from cosmid GG1 f	log pos
Z93784_at	HS398C22	DNA sequence from PAC 398C22 o	log pos

TABLE 10

Urothelium			Other cell types			
Protein	Normal	pTa	pT2+	Leukocytes	Endothelium	Histiocytes
					m	
Keratin 8	+	+	+	-	-	-
CystatinC	+	+	+	+		+
Vimentin	+	-	+		+	
E-cadherin	+	(+)	(+)	?		
CD59	+	(+)	-	+	+	+
					+	
Cathepsin E	-	+	-	+		+
junB	-	+	-	-	-	+
IGF	+	+	-	-	-	-
Beta-2-microglob.	+	+	+	+	+	-
ApoE	+	-	+	-	-	-

CLAIMS

1. A method of determining an expression pattern of a cell sample independent of the proportion of submucosal, smooth muscle, or connective tissue cells present, comprising:
5 determining expression of one or more genes in a sample comprising cells, wherein the one or more genes excludes genes which are expressed in the submucosal, smooth muscle, or connective tissue, whereby a pattern of expression is formed for the sample which is independent of the proportion of submucosal, smooth muscle, or connective tissue cells in the sample.
- 10 2. The method of claim 1 wherein the sample comprises epithelial or carcinoma cells.
3. The method of claim 2 wherein the sample comprises urothelial or bladder cancer cells.
- 15 4. A method of determining an expression pattern of a cell sample, comprising:
determining expression of one or more genes in a sample comprising cells, whereby a first pattern of expression is formed for the sample;
removing expression of genes which are expressed in submucosal, smooth muscle, or connective tissue cells from the first pattern of expression,
20 whereby a second pattern of expression is formed, wherein the second pattern is independent of the proportion of submucosal, smooth muscle, or connective tissue cells in the sample.
5. The method of claim 4 wherein the cell sample is an epithelium or carcinoma sample.
- 25 6. The method of claim 5 wherein the cell sample is a urothelium or bladder cancer sample.
7. A method for determining an expression pattern of a urothelium or bladder cancer cell, comprising:
determining expression of one or more genes in a sample comprising
30 urothelium or bladder cancer cells, whereby a first pattern of expression is formed;

subtracting from the first pattern of expression a second pattern of expression, wherein the second pattern was formed using the one or more genes and a sample comprising predominantly submucosal, smooth muscle, or connective tissue cells, said step of subtracting forming a third pattern of expression which reflects expression of the urothelium or bladder cancer cells independent of the proportion of submucosal, smooth muscle, or connective tissue cells present in the sample.

8. A method of detecting an invasive tumor in a patient, comprising:

detecting in a sample of a body fluid a marker which is more prevalent in submucosal, smooth muscle, or connective tissue than in the body fluid, wherein the marker is an mRNA or protein expression product of a gene, wherein an increased amount of the marker in the body fluid indicates a tumor which has become invasive in the patient.

9. The method of claim 8 wherein the body fluid is selected from the group consisting of blood, plasma, serum, urine, ascites fluid, pleural fluid, spinal fluid, sputum, and mucous secretions.

10. The method of claim 8 wherein the marker is a protein characteristic of submucosal, smooth muscle, or connective tissue, but not found in the body fluid.

11. A method to diagnose a bladder cancer comprising:

determining a first pattern of expression of one or more genes in a bladder tissue sample suspected of being neoplastic;

comparing the first pattern of expression to a second and third reference pattern of expression, wherein the second pattern is of the one or more genes in normal urothelium and the third pattern is of the one or more genes in bladder cancer, wherein a first pattern of expression which is more similar to the third pattern than the second indicates neoplasia of the bladder tissue sample.

12. A method to predict outcome or prescribe treatment of a bladder tumor, comprising:

determining a first pattern of expression of one or more genes in a bladder tumor sample;

5 comparing the first pattern to one or more reference patterns of expression determined for bladder tumors at grades I to IV;

determining which of the reference patterns shares maximum similarity with the first pattern, wherein the outcome or treatment appropriate for the grade of tumor of the reference pattern with the maximum similarity is assigned to the bladder tumor sample.

10 13. A method to determine grade of a bladder tumor, comprising:
determining a first pattern of expression of one or more genes in a bladder tumor sample;

15 comparing the first pattern to one or more reference patterns of expression determined for bladder tumors at grades I to IV;

determining which of the reference patterns shares maximum similarity with the first pattern, wherein the grade of the reference pattern with the maximum similarity is assigned to the bladder tumor sample.

20 14. A method to determine stage of a bladder tumor, comprising:
determining a first pattern of expression of one or more genes in a bladder tumor sample;

comparing the first pattern to one or more stage-specific reference patterns;

25 determining which of the stage-specific reference patterns shares maximum similarity with the first pattern, wherein the stage of the reference pattern with the maximum similarity is assigned to the bladder tumor sample.

30 15. The method of claim 14 wherein the pattern of expression of the bladder tumor sample and the reference patterns comprise data on the expression of one or more genes selected from the group consisting of TCC-related genes, bladder papilloma-related genes, and invasive TCC-related genes.

16. A method of identifying a tissue sample as urothelial,
comprising:

determining a first pattern of expression of one or more genes in a
tissue sample;

5 comparing the first pattern of expression to a second pattern of
expression obtained from normal urothelial cells; wherein similarity between
the first and second patterns identifies the tissue sample as urothelial in its
origin.

17. The method of claim 16 further comprising the step of:
10 comparing the first pattern to one or more third patterns of expression
obtained from other cell types, wherein differences between the first
and third patterns confirms the suggestion that the tissue sample is
urothelial in origin.

18. A method to identify a set of genes useful for diagnosing,
15 predicting outcome, or prescribing treatment of a bladder
cancer comprising:

determining a first pattern of expression of one or more genes in a first
bladder tissue sample;

20 determining a second pattern of expression of the one or more genes
in a second bladder tissue sample, wherein the first bladder tissue sample is a
normal urothelium sample or an earlier stage or lower grade of bladder tumor
than the second bladder tissue sample;

25 comparing the first pattern of expression to the second pattern of
expression to identify a first set of genes whose expression is increased or
decreased in the second bladder tissue sample relative to the first bladder tissue
sample;

30 removing from the first set of genes those genes which are expressed
in submucosal, smooth muscle or connective tissue to produce a second set of
genes, wherein measurement of expression of the second set of genes can be
used for diagnosing, predicting outcome, or prescribing treatment of a bladder
cancer.

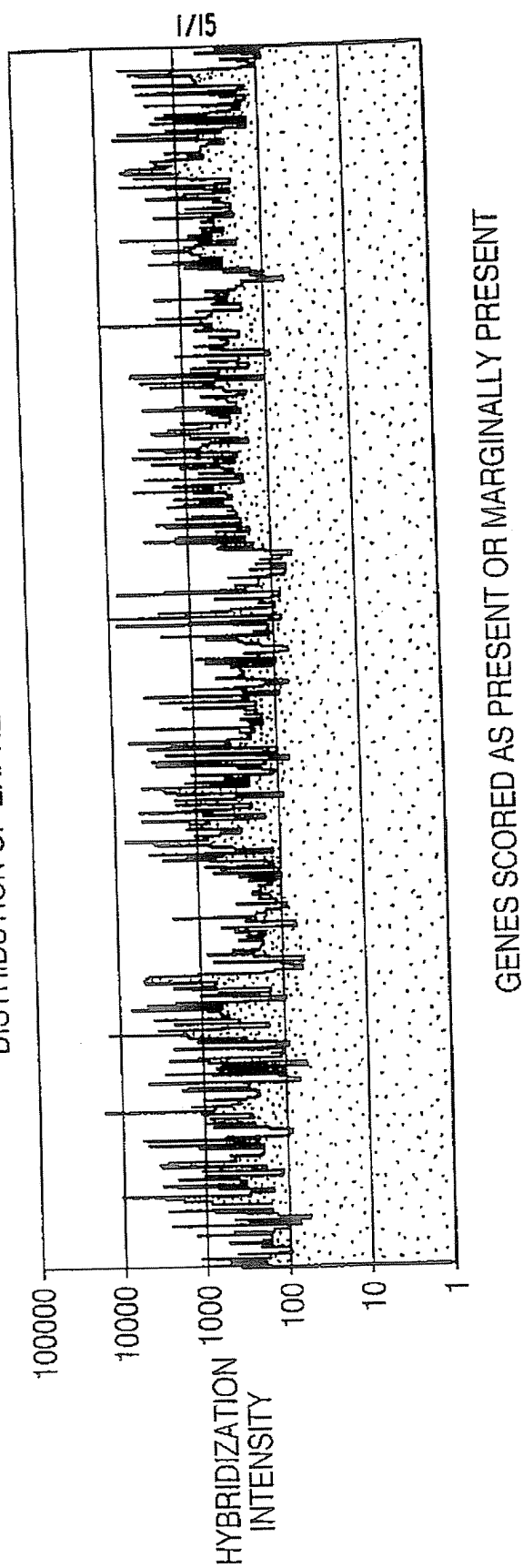
19. A method of determining an expression pattern of a bladder tissue sample independent of the proportion of submucosal, smooth muscle, or connective tissue cells present, comprising:
isolating a single-cell suspension of disaggregated bladder tumor cells
5 from a bladder tissue sample comprising bladder cells, and cells of one or more of a cell type selected from the group consisting of submucosal cells, smooth muscle cells, or connective tissue cells;
determining expression of one or more genes in the single-cell suspension, whereby a pattern of expression is formed for the sample which is
10 independent of the proportion of submucosal, smooth muscle, or connective tissue cells in the bladder tissue sample.
20. The method of any of claims 1-19 wherein expression of a gene is determined by assaying for an mRNA transcribed from the gene or a protein translated from an mRNA transcribed from the gene.
15
21. The method of any of claims 1-19 wherein expression of a plurality of genes is determined.
22. A method of screening for candidate therapeutic agents for treating bladder cancer, comprising the steps of:
20 contacting bladder tumor cells with a test compound;
determining gene expression of one or more genes in the bladder tumor cells which have been contacted with the test compound, wherein expression of the one or more genes changes during the development of a bladder cancer;
identifying a test compound as a candidate therapeutic agent if it causes
25 gene expression of at least one of the one or more genes to change to a level which is characteristic of an earlier stage of cancer progression.
23. A method of categorizing a tumor, comprising the steps of:
mixing cells of a plurality of tumors, wherein the tumors are of a single type and of a similar stage or grade to form a pool;
30 determining expression of one or more genes in the pool;

comparing expression of the one or more genes in the pool to expression in a test sample derived from a tumor, wherein similarities between the test sample expression and the pool expression permit categorization of the tumor.

- 5 24. A method of categorizing a tumor, comprising the steps of:
 mixing one or more gene products from cells of a plurality of
tumors, wherein the tumors are of a single type and of a similar stage or grade
to form a pool, wherein the gene product is mRNA or protein;
 determining expression of one or more genes in the pool by
10 assaying the gene product in the pool;
 comparing expression of the one or more genes in the pool to
expression in a test sample derived from a tumor, wherein similarities between
the test sample expression and the pool expression permit categorization of the
tumor.
- 15 25. A method of categorizing a tumor, comprising the steps of:
 determining expression of one or more genes in a plurality of
tumors, wherein the tumors are of a single type and of a similar stage or grade;
 combining data determined for the expression of the one or
more genes to form a data pool;
20 comparing expression of the one or more genes in the data pool
to expression in a test sample derived from a tumor, wherein similarities
between the test sample expression and the data pool permit categorization of
the tumor.
- 25 26. The method of claim 23, 24, or 25 wherein the tumors are
bladder tumors.

FIG. 1

DISTRIBUTION OF EXPRESSION LEVELS IN BLADDER WALL

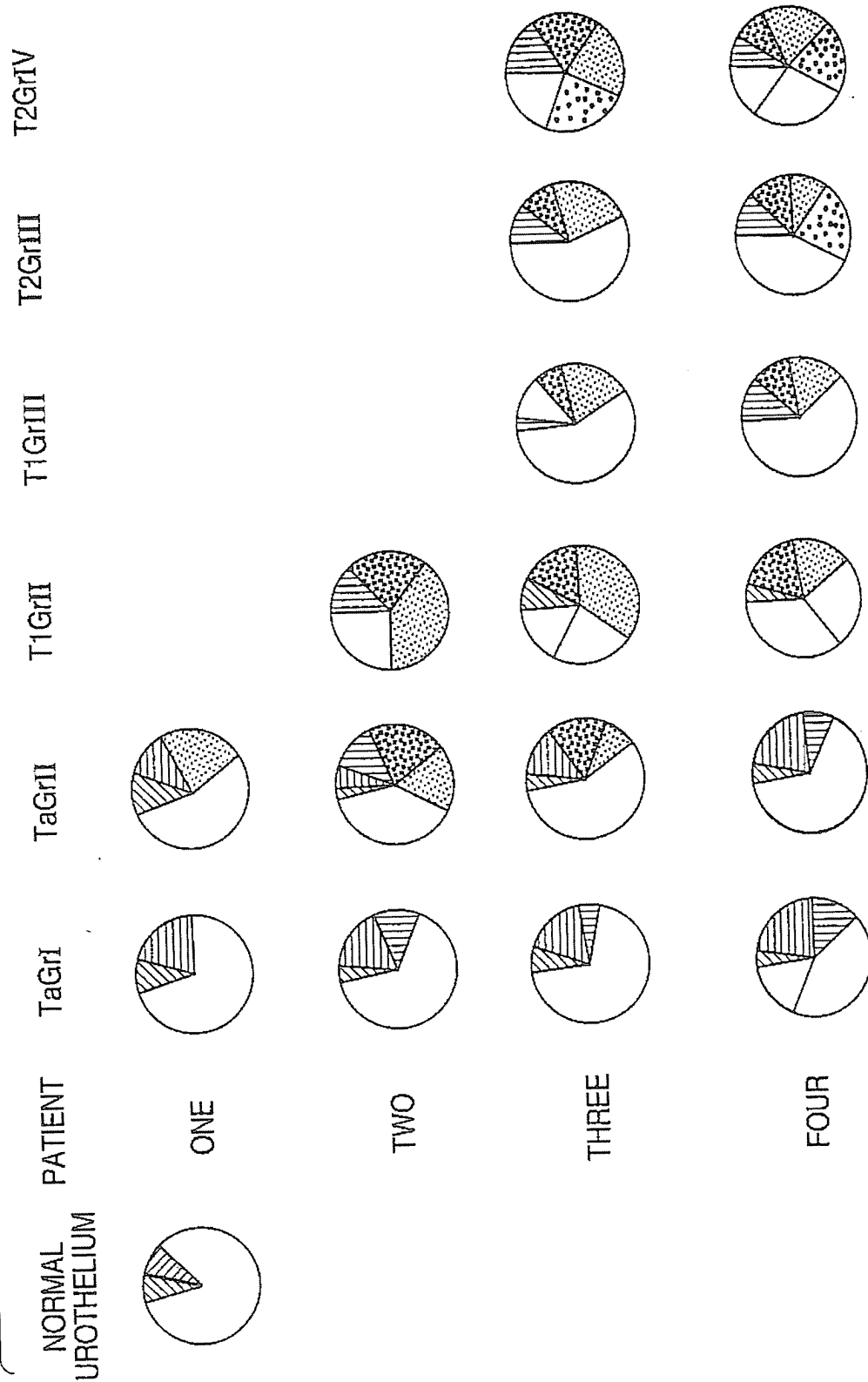


2/15

Fig. 2 was missing at the time of publication

3/15

FIG.3



4/15

FIG. 4A

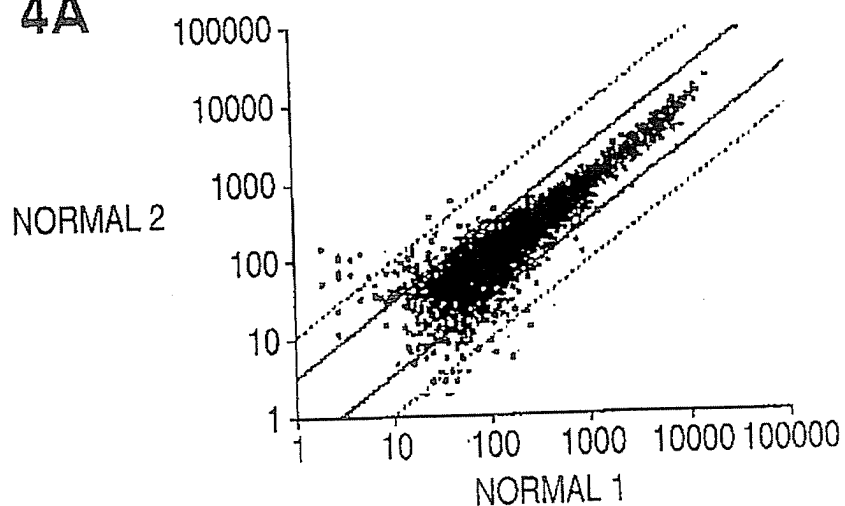


FIG. 4B

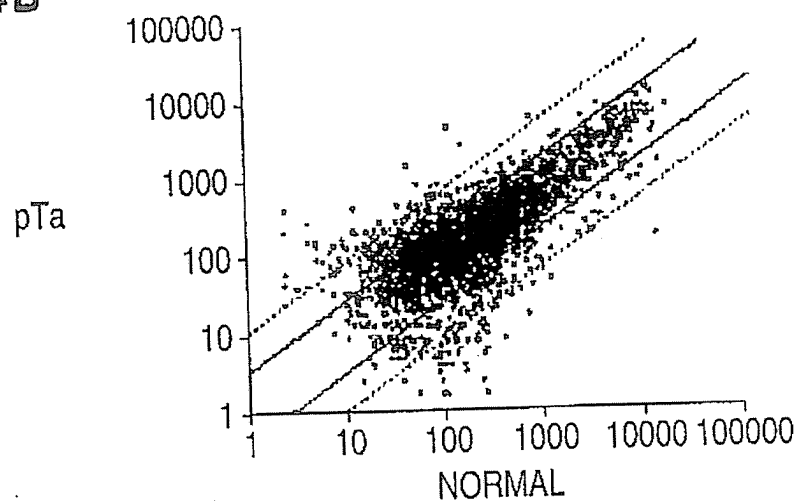
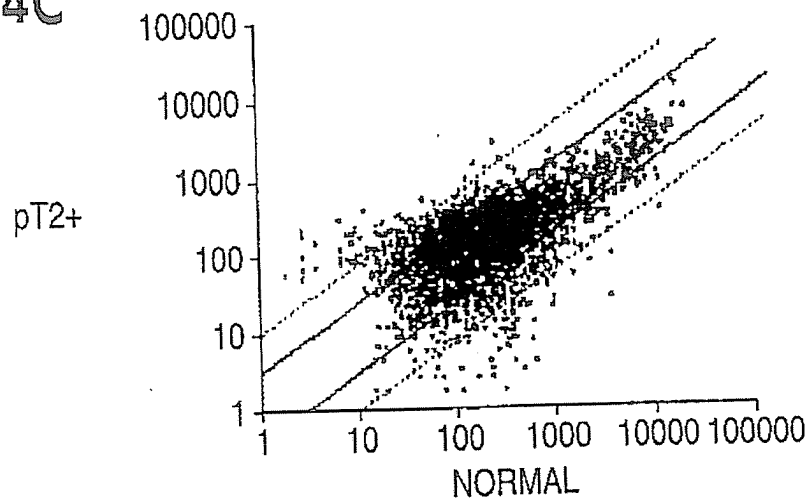


FIG. 4C



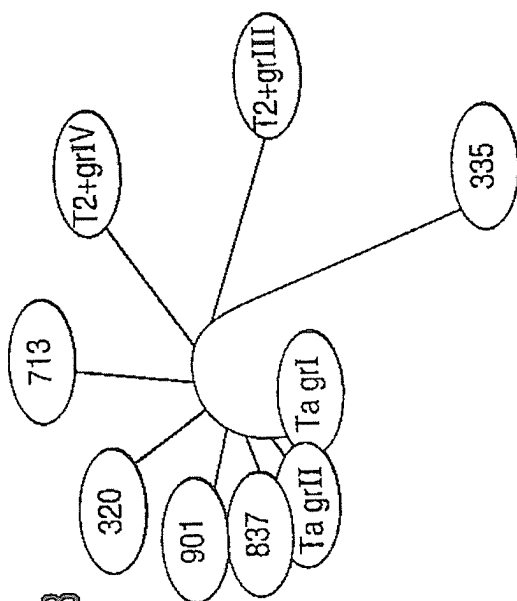


FIG. 5B

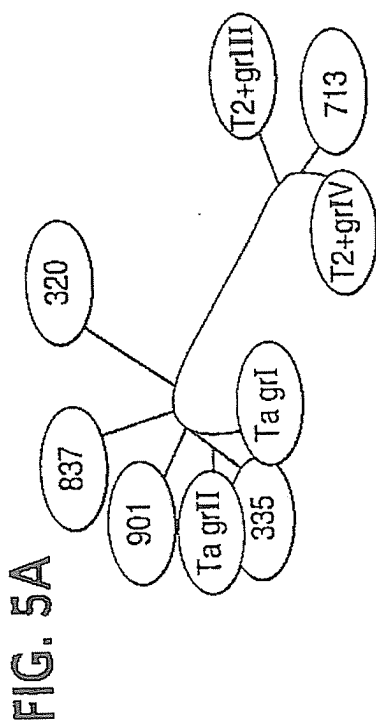


FIG. 5A

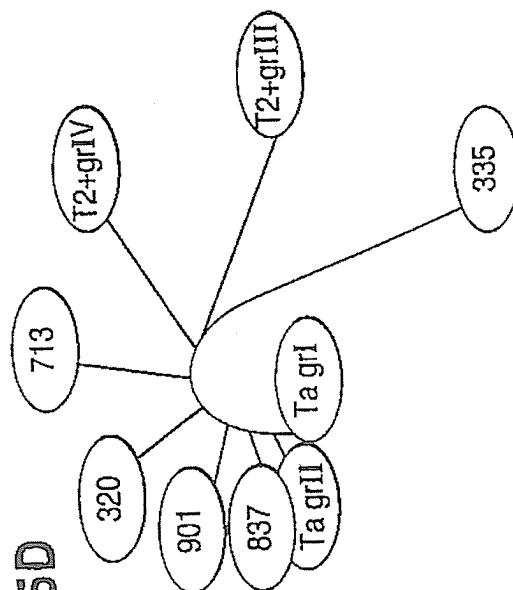


FIG. 5D

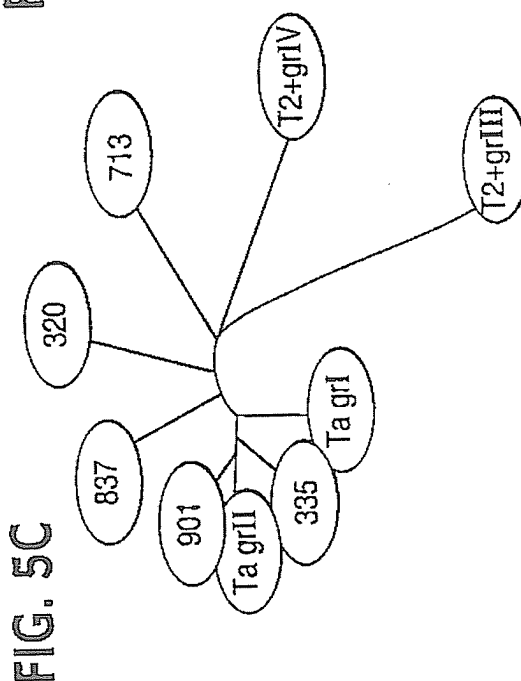
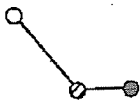


FIG. 5C

FIG. 6A

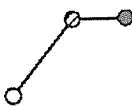
6/15
TCC related genes



A.

M12125	Tropomyosin
D00654	Smooth muscle gamma-Actin
X04470	Antileukoprotease (ALP)
U08021	Nicotinamide N-methyltransferase (NNMT)
M16276	MHC class II HLA-DR2-Dw12
K02765	Complement component C3
J02854	Myosin light chain (MLC-2)
J05582	Pancreatic mucin
D17408	Calponin
M95787	Smooth muscle protein (SM22)
X99133	NGAL gene
M31951	Perforin (PRF1)
HG3431-HT3616	Decorin
S75256	Neutrophil lipocalin (HNL)
X13839	Smooth muscle alpha-Actin
M84526	Adipsin/complement factor D
AF001548	Chromosome 16 BAC clone CIT987SK-815A9

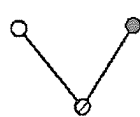
FIG. 6B



B.

M13955	Keratin K7 (type II)
D87953	RTP
HG3543-HT3739	Insulin-Like Growth Factor 2

FIG. 6C



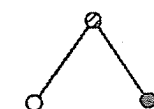
Bladder papilloma related genes

C.

M63438	Ig rearranged gamma chain V-J-C region and complete cds
M25079	Sickle cell beta-globin
Z84721	Human DNA sequence 2Mb contig from cosmid GG1
X00274	HLA-DR alpha heavy chain a class II antigen
X57809	Rearranged immunoglobulin lambda light chain
M34516	Human omega light chain protein 14.1
M13560	Ia-associated invariant gamma-chain gene
L02326	Clone Hu lambda-17
M33600	MHC class II HLA-DR-beta-1 (HLA-DRB1)
HG1428-HT1428	"Globin Beta"
V00594	Metallothionein
X57351	1-8D gene from interferon-inducible gene family
S71043	Ig alpha 2=immunoglobulin A heavy chain allotype 2
M87789	"Human (hybridoma H210) anti-hepatitis A IgG
M12529	Human apolipoprotein E
HG3576-HT3779	MHC Class II Beta W52
M57466	MHC class II HLA-DP light chain
Z19554	Vimentin gene
X03068	HLA-D class II antigen DQw1.1 beta chain
J04164	Interferon-inducible protein 27-Sep
X17042	MRNA for hematopoietic proteoglycan core protein
M55998	Alpha-1 collagen type I

7/15

FIG. 6D

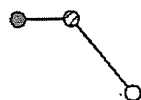


J03242
U20734
X64364
L12711
M32053
M17863
X15573
M22430
M84424
X59798
X07696
M94856

D.

Insulin-like growth factor II
Transcription factor junB
MRNA for M6 antigen
Transketolase (tk)
H19 RNA "gene"
Preproinsulin-like growth factor II (IGF-II)
Liver-type 1-phosphofructokinase (PFKL)
RASf-A PLA2
Cathepsin E (CTSE)
PRAD1 mRNA for cyclin
MRNA for cytokeratin 15
Human fatty acid binding protein homologue (PA-FABP)

FIG. 6E



M62403
J04093
X12876
L19686
AC002115
M55409
U12404
Z28407
X93036
X98482
X82693
AF000562
U16799
X54232
J02874
L76568
M65292
L33842
U24389
X76180
D63475
D16480

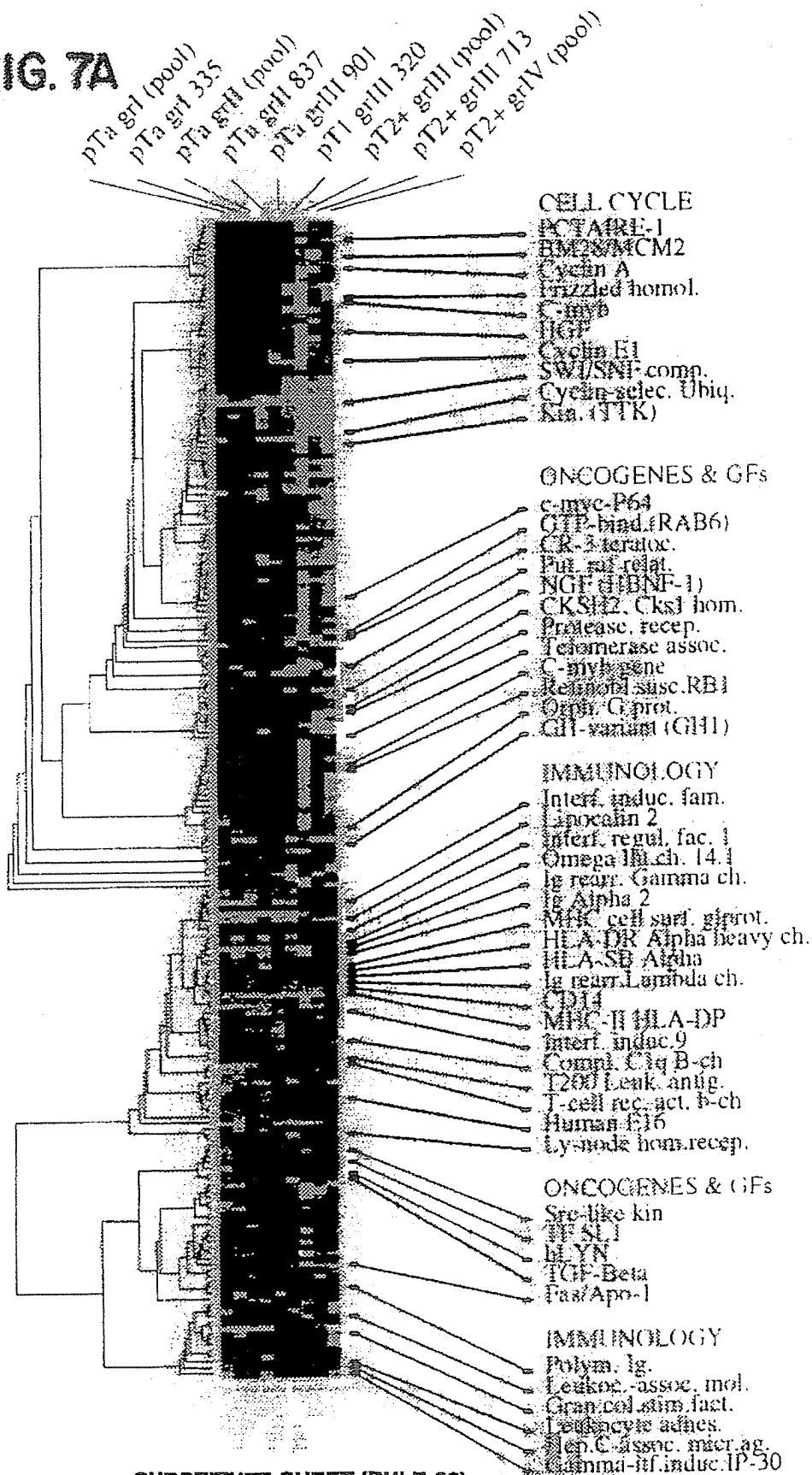
Invasive TCC related genes

E.

Insulin-like growth factor binding protein 4 (IGFBP4)
Phenol UDP-glucuronosyltransferase (UDPGT)
DNA seq. From RP3-474112 on chromosome 22q13.1-13.2
Macrophage migration inhibitory factor
DNA from chr. 19 cosmids R31396, F25451, and R31076
Pancreatic tumor-related protein
Human Csa-19
MRNA for ribosomal protein L8
MRNA for MAT8 protein
TNNT2 gene exon 11
MRNA for E48 antigen
Uroplakin II
Na,K-ATPase beta-1 subunit
MRNA for heparan sulfate proteoglycan (glypican)
Adipocyte lipid-binding protein
S26 from excision and cross link repair protein (ERCC4)
Human factor H homologue
Type II inosine monophosphate dehydrogenase (IMPDH2)
Lysyl oxidase-like protein gene
MRNA for lung amiloride sensitive Na⁺ channel protein
MRNA for KIAA0109
Mitochondrial enoyl-CoA hydratase/3-hydroxyacyl-CoA dehydrogenase

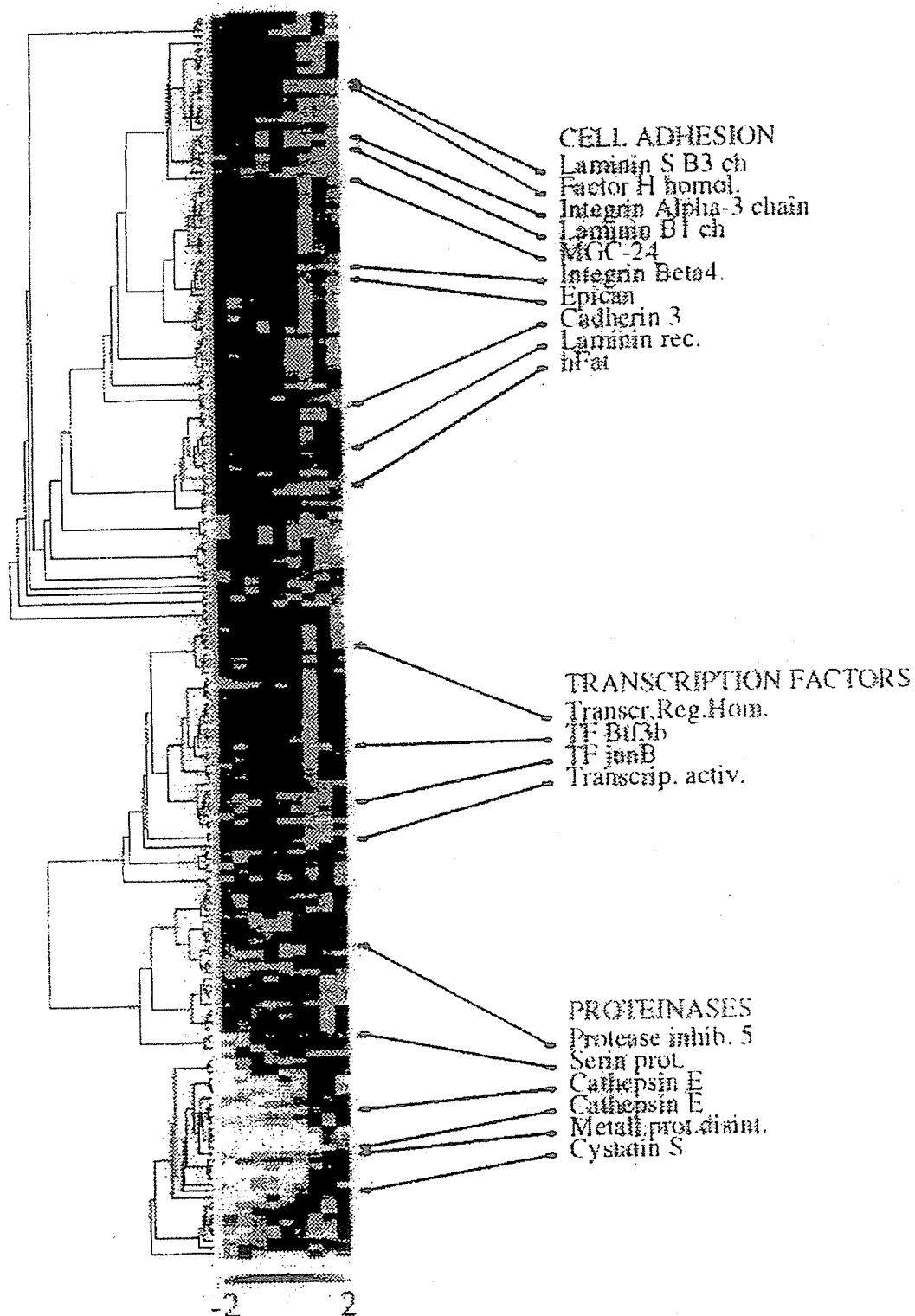
8/15

FIG. 7A



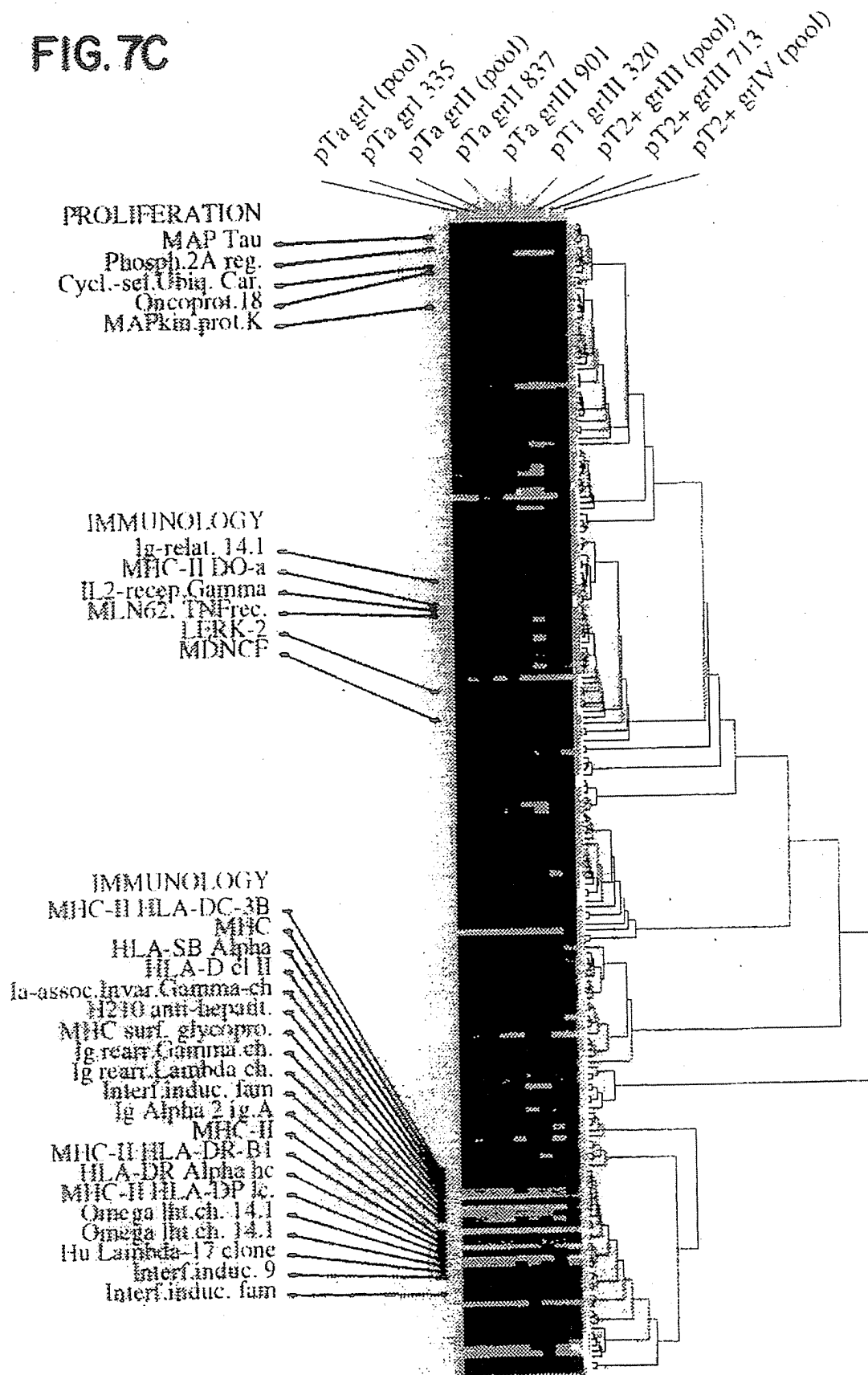
9/15

FIG. 7B



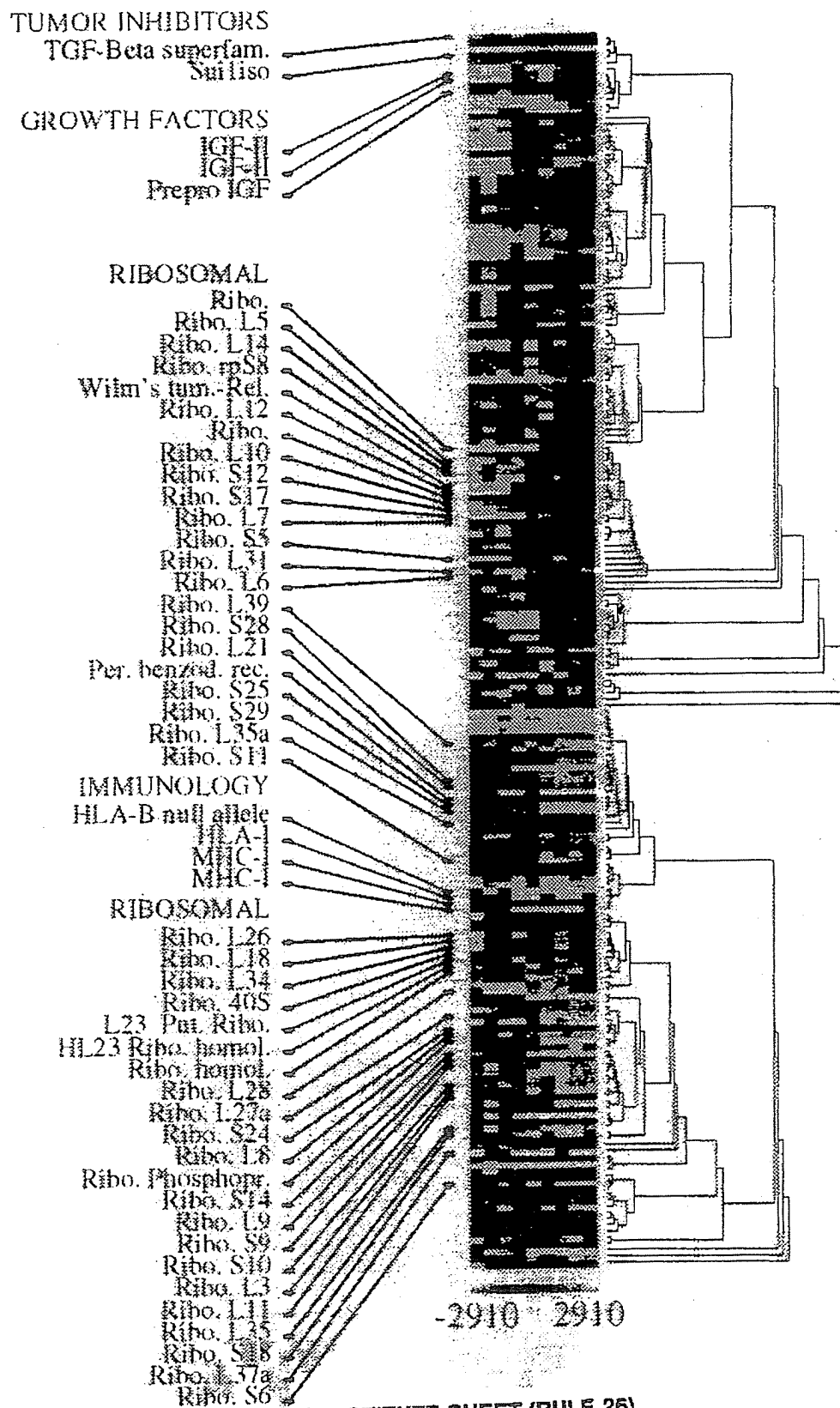
10/15

FIG. 7C



11/15

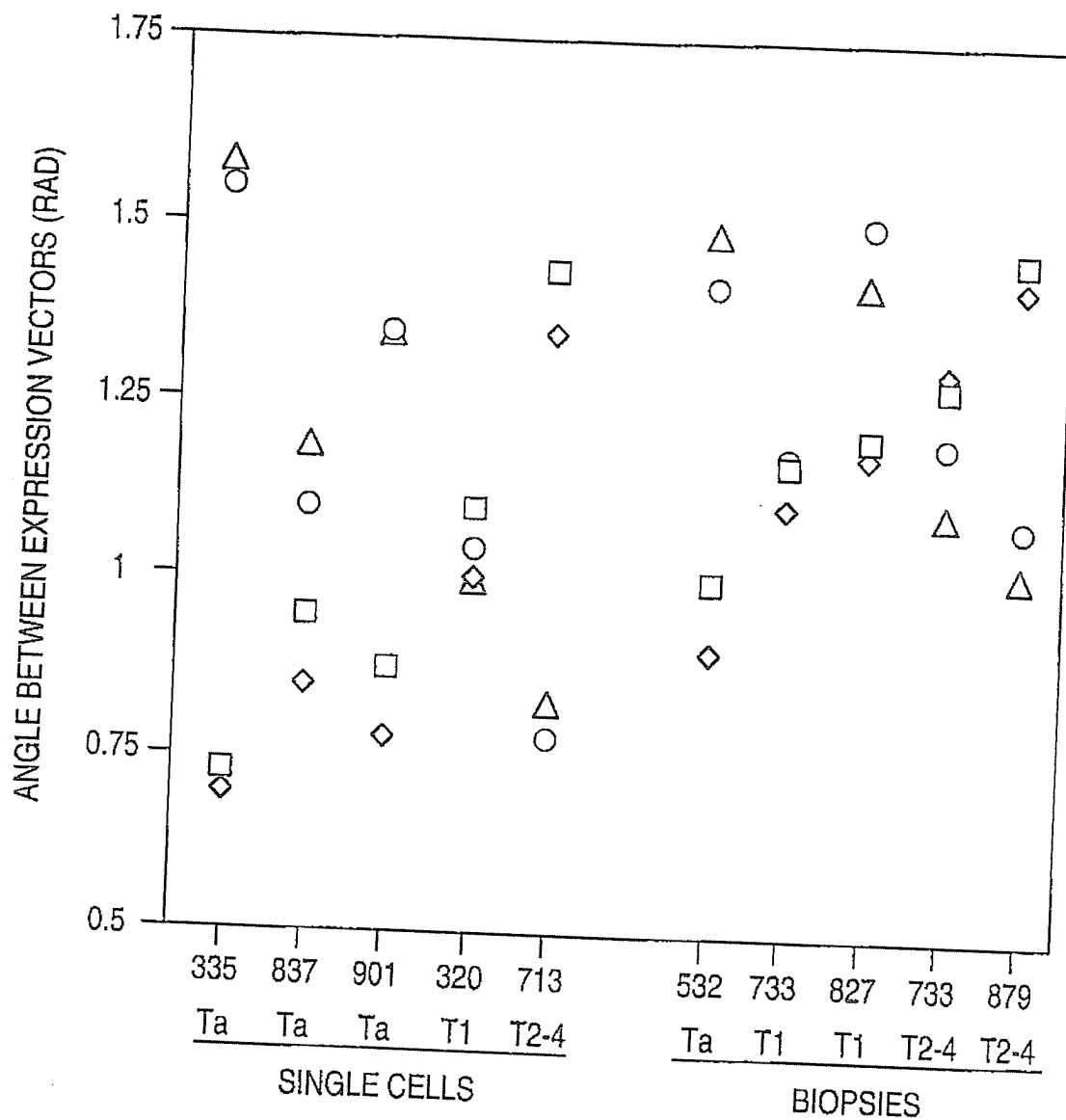
FIG. 7D



SUBSTITUTE SHEET (RULE 26)

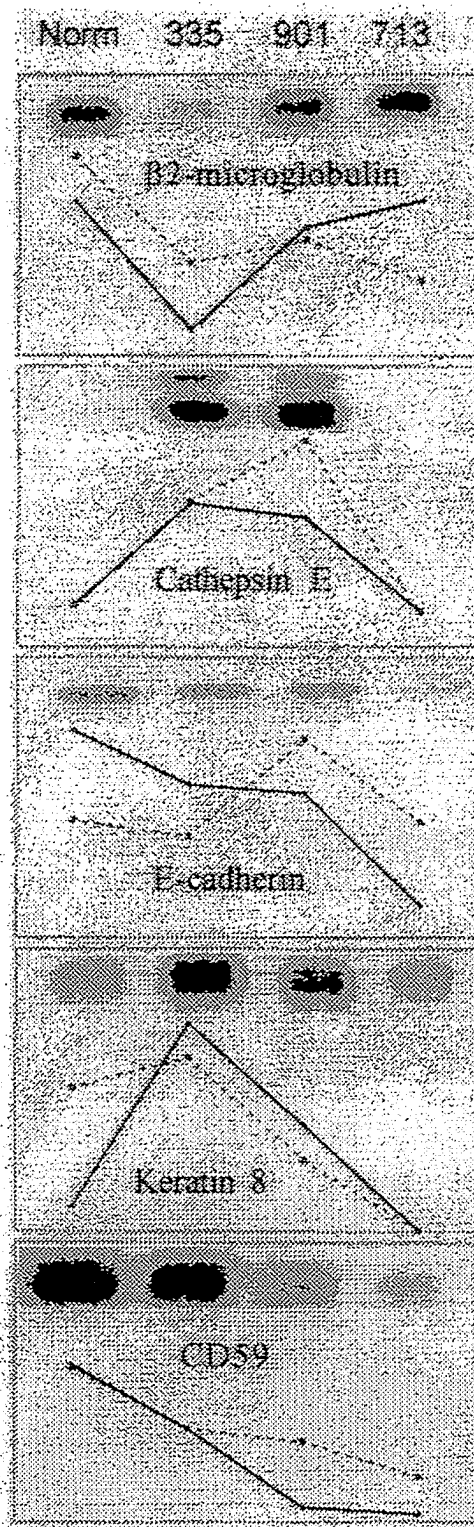
12/15

FIG. 8



13/15

FIG. 9



14/15

FIG. 10



15/15

Fig. 11 was missing at the time of publication